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# Variability in genome editing outcomes: challenges for research reproducibility and clinical safety

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## Abstract

Genome editing tools have already revolutionised biomedical research and are also expected to have an important impact in the clinic. However, their extensive use in research has revealed much unpredictability, both off- and on-target, in the outcome of their application. We discuss the challenges associated with this unpredictability, both for research and in the clinic. For the former, an extensive validation of the model is essential. For the latter, potential unpredicted activity does not preclude the use of these tools but requires that molecular evidence to underpin the relevant risk:benefit evaluation is available. Safe and successful clinical application will also depend on the mode of delivery and the cellular context.

## Keywords

Functional genomics, Gene delivery, Gene therapy, CRISPR/Cas9, Medical research, Clinical safety, Research reproducibility

## Introduction

New therapies that employ genome editing tools (GETs) are being developed for a broad range of disease including cancers,  $\beta$ -thalassemia, sickle cell disease and Duchenne muscular dystrophy (reviewed and discussed in <sup>1-6</sup>). Meanwhile, although GETs are efficient at inducing specific double-strand breaks (DSBs), the outcome of DNA repair remains unpredictable. Validation of edited models, checking both targeted allele and potential off-target (OT) changes, is therefore essential to ensure research reproducibility. With more than 30 clinical trials underway or concluded<sup>1</sup>, the safety and efficacy of GETs as therapeutic agents are being explored. The safety challenges associated with using these tools (see Box 1 for key messages) and potential solutions are discussed in this review.

### Off-target effects: the tip of the iceberg?

Closely associated with the efficacy to target specific genomic sequences is the risk of generating unwanted mutations. Until recently, OT cuts have been the main focus of discussions: initial use of GETs on human cultured cells raised concerns about the specificity that could be achieved, as frequent OT cutting events were recorded <sup>7-10</sup>. Subsequent studies of CRISPR/Cas9 unwanted effects suggested that, in mice, OT events were rare <sup>11-13</sup>. The same conclusion was reached in various other models: tomato <sup>14</sup>, rice <sup>15,16</sup>, Arabidopsis <sup>17</sup>, zebrafish <sup>18</sup> and human cell culture models <sup>19-24</sup>, and with the use of TALENs <sup>20,21</sup>. The conclusion of these studies was challenged by Schaeffer and colleagues who reported frequent and unexpected types of genetic variations in a published article that was subsequently withdrawn when its methodology came under scrutiny <sup>25</sup>. It is noteworthy that, with the exception of this retracted paper, high frequency OT effects have most commonly been reported in cell culture with sustained Cas9/guide expression <sup>7,8,10,24,26</sup>. The level of expression achieved, genetic impact of maintaining cells in culture, transfection method, cell type, guide sequence, constitutive nuclease expression or a combination of any of these factors may explain the differences between high and low

frequency of OT events. More recent studies <sup>11,27-31</sup> reinforce the conclusion that the frequency of OT effects when GETs are used *in vivo* is lower than the natural occurrence of genetic drift <sup>32</sup>.

Less highlighted, but more important, is the variety of repair events that occur subsequent to DSBs on target. Evidence of CRISPR/Cas9-triggered genomic rearrangements was published early in their use <sup>33</sup> and related potential safety issues for patients in therapeutic settings were largely unnoticed. Further work demonstrated that DSBs by one or more single-guide ribonucleic acids (sgRNAs) also led to a high frequency of various and sometimes complex (and often unwanted) events in a range of cellular contexts (early embryos, embryonic stem cells, primary cultures and established cell lines) <sup>33-41</sup>: these included deletions larger than the genomic segments defined by the sgRNAs, duplications (see examples in <sup>34,40</sup>), inversions (examples in <sup>34,40</sup>), insertions of unrelated DNA sequences<sup>41</sup>, translocations (examples in <sup>35</sup>) and combinations of these rearrangements <sup>33-35,37,39</sup>. But overall, the most common unexpected repair event that was described was a deletion of a small number of kilobases around the site of CRISPR/Cas9 nuclease or nickase activity <sup>36,42</sup>. Unexpected sequence rearrangements may potentially induce confounding phenotypes; for example, an initially unrecognized bystander tandem duplication associated with an enhancer deletion allele in *Ilr2a* causes immune dysregulation through increased cellularity and relative representation of memory T cells <sup>43</sup>.

With the addition of donor templates, the complexity of repair outcomes increases, as the donor sequence also may integrate partially or incorrectly <sup>44-46</sup>. Recently deep scanning of large numbers of events in cell culture with long-read sequencing illustrated the diversity of repair obtained, with a knock-in attempt resulting in a complex population of indels and partial, rearranged or concatemerised on-target donor insertion, in addition to the expected integration event <sup>47</sup>. Furthermore, OT donor integrations (partial or integral) are not uncommon with both double- and single-stranded DNA templates alike <sup>44,46</sup>.

The precise DNA repair mechanisms that yield this vast variety of repair events are largely unknown. DSBs are highly toxic events <sup>48</sup> and elicit cellular responses (for example, p53-mediated DNA damage response and cell cycle arrest <sup>49,50</sup>). One of several possible complex repair mechanisms is induced <sup>51,52</sup>, which most likely determines the resulting repair event. Examples of such potential consequences may include unintentional mutations in the cancer driver genes *VHL* or *KRAS*, as a result of GET activity yielding neoplastic events <sup>53</sup>. More intense research is needed to understand, and perhaps in the future control, which repair pathway is activated following DNA cutting by GETs. In this context, as molecules that increase the frequency or extent of mutations, GETs fit the definition of 'targeted mutagens'. Therefore, it is unrealistic to expect that GETs alone will guarantee the desired outcomes of their use. In conclusion, whether they are used alone or in combination with donor templates, although GETs are astonishingly efficient at generating sought-after sequence changes, which DNA repair mechanisms are triggered is poorly understood and even less well controlled. On-target variability has been understudied. The gravity of the risks associated with it will depend on the biological function of modified loci. In addition, this variability also means that the desired sequence may not be obtained, preventing the generation of the mutation of interest or the achievement of the therapeutic goal. In the biomedical research setting, these findings highlight challenges for ensuring research reproducibility (see following paragraph). In the clinic, the emphasis turns to evaluating the benefit-to-risk ratio of gene editing therapy, including considering the full range of possible outcomes.

#### [Reproducibility studies in basic and preclinical research informs clinical strategies](#)

The variability of GET-induced mutations described in the previous paragraph emphasizes the importance of experimental design in considering the possibility of unexpected outcomes of DSB repair, differentiating it from the effect of genetic drift<sup>27-31</sup>, and to exclude unwanted events during the validation of genome-edited models, whether in cell culture or in animals. In particular, it is recognized that insufficient molecular validation

of *in vivo* models plays an important role in the misinterpretation of scientific results <sup>54</sup>. To be explicit, detailed characterization of the models generated by GETs is required to ensure research validity.

With the apparent ease of generating mutated founder animals, the first generation produced by the action of GETs in embryos was initially heralded as a desirable model for phenotyping <sup>55</sup>. However, it is now clear that the founder generation may only be used for specific phenotypic screens <sup>56</sup>. Association of a biological trait to a specific genetic variation requires the mutation to be established and validated in generations subsequent to the founder stage, to exclude any unpredicted on-target events. Additionally, repeated crossing of the GET-generated mutant with wild-type animals will segregate most OT mutations, thus lowering the likelihood that phenotypes could be caused by OT rather than on-target sequence changes.

Importantly, understanding and controlling the variability of the outcome of GET use in laboratory animals is informing the clinical field on potential undesired effects and will provide solutions to deal with these risks. However, full assessment of GET activity and of its impact will await clinical trial results.

### What is already known in humans?

Early therapeutic attempts to use GETs in humans employed zinc finger nucleases (ZFNs), targeting the *CCR5* gene for the treatment of HIV-infected patients <sup>58</sup>. The same strategy has now been tested in both autologous T cells and HSCs without genotoxic side effects. The first direct DNA modification using ZFNs involved adeno-associated virus (AAV)-mediated *in vivo* delivery for the treatment of Hunter metabolic disease <sup>59</sup>. After four months, in the two men who received the highest dose, glycosaminoglycan sugar levels dropped substantially, but iduronate 2-sulfatase – the enzyme that breaks these sugars and is not functional in Hunter syndrome – remained undetected in blood and, furthermore, no signatures of genome-edited tissue were recovered <sup>60</sup>. These results are

therefore difficult to interpret in terms of the safety and efficacy of this therapy and are not conclusive.

TALENs were also employed to engineer universal chimeric antigen receptor T cells by disruption of T-cell receptor (*TCR*) and *CD52* genes, leading to remission of acute lymphocytic leukemia in two one-year-old infants <sup>61,62</sup>. The cells were used in a time-limited manner to obviate safety concerns and no genotoxic side effects were detected. Over 20 subjects have since been treated using similar cells with no TALEN-related toxicity described <sup>63</sup>. Of note, in these multiplex edited cells, the risk of translocations between edited chromosomes was recognized and quantified <sup>64</sup>.

The first studies employing ex vivo CRISPR modified cells have been initiated in China with the ex vivo targeting of the programmed cell death protein 1 gene (*PDCD1*) in T cells of patients with metastatic non-small cell lung cancer <sup>65</sup> followed by infusion of the cells back into patients. However, clinical data have not been published. A number of additional studies modifying TCR, human leukocyte antigen (HLA) class I and *PDCD1* using CRISPR/Cas9 editing have been reviewed by regulatory agencies. The first results of a phase I human clinical trial with patients suffering from refractory cancer were published very recently <sup>66</sup>. The authors showed persistence of the engraftment of cells with edits in three loci *TRAC*, *TRBC* and *PDCD1* after nine months, showing the feasibility of such therapy for cancer immunotherapy. The trial identified no safety issues, although it also illustrated genetic heterogeneity in the grafted cells, including chromosomal translocations.

Other studies had addressed the possibility of initiating HIV resistance through the modification of *CCR5* <sup>67</sup>. Although the therapeutic goal was not met, no issues of immune reaction or other adverse effects were reported <sup>67,68</sup>.

Injection of CRISPR/Cas9 modified CD34+ HSCs was shown to ameliorate the pathology of both sickle-cell disease and  $\beta$ -thalassaemia <sup>69</sup>. A first *in vivo* CRISPR/Cas9 trial, administered via subretinal injection, was launched in March 2019 to treat an inherited



form of blindness caused by a mutation in the *CEP290* gene (NCT03872479;<sup>3,6</sup>). These trials herald promise for the use of GE for tissue engineering or somatic therapies.

In November 2018, the announcement of the alteration of the genome of twin girls using CRISPR/Cas9 in human early-stage embryos shocked the scientific community <sup>70</sup>. This first gametic trial raised major practical and ethical concerns, around both the absence of full scientific evaluation and licencing, and the safety and efficacy of *CCR5* gene inactivation to prevent HIV infection, but chiefly about the ethically contentious use of GET for human germline modification and the potential for a drift towards eugenism.

Today over 30 GET trials are registered on ClinicalTrials.gov but not all will reach patient recruitment <sup>1</sup>. However, few data on short-term toxicity <sup>58,61</sup> and no data on long-term toxicity are yet available. Early *in vivo* or *ex vivo* GET trials are either to assess safety in healthy individuals or are mostly fast-tracked studies of therapy for terminally ill patients.

#### Threshold of benefit:risk analysis

As described above, GETs, along with other therapeutic tools ranging from radiotherapy <sup>71</sup> and chemotherapy <sup>71</sup> to integrating viral vectors, inherently carry risks of genotoxicity. Both radiotherapy and chemotherapy cause random genomic alterations, from single nucleotide changes to large-scale chromosomal rearrangements. The application of gamma-retroviral vectors for the modification of hematopoietic stem cells (HSCs) in children with inherited severe combined immunodeficiency (SCIDX1) resulted in serious adverse effects from insertional mutagenesis <sup>72</sup>. Similar complications were later reported in chronic granulomatous disease <sup>73</sup> and Wiskott-Aldrich syndrome <sup>74</sup>. The issue seems to have been resolved by switching to self-inactivating lentiviral<sup>75</sup> and gamma-retrovirus<sup>76</sup> with deleted LTR U3 enhancer sequences. Interestingly, variations remain between disease settings, with no transformation events reported for the enzyme deficiency adenosine deaminase SCID <sup>77</sup>. Other conditions, in which carefully regulated gene expression is likely to be required to avoid transformation, have not, to date, been

tackled by 'gene-addition' strategies, but could be well suited to GETs. In addition, the nature of the target cells being modified is critical, with reported genotoxicity limited to studies modifying stem cells and no similar occurrences in other *ex-vivo* modified T cells, keratinocytes or fibroblasts <sup>78</sup>. Alternative non-viral systems, such as the sleeping beauty transposon gene delivery platform, have also reached clinical phase testing <sup>64</sup>. Constitutive expression of transposase was known to be highly mutagenic, and yet transient expression during *ex-vivo* modification of cells has, to date, been safe.

GETs only affect specific targets and, potentially, a small number of DNA sequences with a high degree of homology. Furthermore, GETs represent a heterogeneous group and differ in efficiency and target specificity <sup>79</sup>. Therefore, each GET carries specific risks, in terms of both the frequency of the target and highly related sequences, and the specific risks attached to the targets' loci <sup>80</sup>.

For clinical use, the mode of delivery of GETs influences the risks and depends, among other factors, on whether the genetic defects have a somatic or developmental etiology. Depending on this, therapy will involve tissue engineering and somatic delivery or may require germline intervention, each of which bring fundamentally different challenges. Efficiency and safety with each given delivery mode for use in the clinic must be validated together for any genome editing-based therapeutic intervention (for reviews on delivery see <sup>81,82</sup>). As with any other therapeutic agent, the delivery mode itself of GETs brings inherent safety risks: viruses can be associated with a high risk of gene disruption <sup>83</sup> or can cause problems of toxicity and immunogenicity <sup>84</sup>. Likewise, transfer of naked DNA to cells is known to activate an immune response<sup>85</sup>.

Delivery of any new DNA into a cell has the potential to generate unexpected genomic sequence insertions.

In conclusion, defining the risk by nuclease type (that is, ZFN, TALEN or CRISPR/Cas9) is not possible. The initial perception of these molecules was that of an entirely specific and predictable family of tools. Potential secondary effects have since been revealed and

earlier over-optimistic expectations have been shattered, leading to debate over the risks associated with the use of GETs.

In light of the benefits expected from the use of GETs, some cancer risk may become acceptable for lethal diseases such as Duchenne muscular dystrophy, for which the use of CRISPR/Cas9 may show promise<sup>86</sup> and numerous preclinical studies are ongoing<sup>87</sup>. Already, clinical trials to treat refractory cancer are also underway<sup>66</sup>. But for less immediately critical conditions, such as human immunodeficiency virus (HIV) infection<sup>88</sup>, the threshold of acceptability will be different. Overall, relevant risks for potential secondary cancer development or for other adverse effects remain to be evaluated.

#### Clinical risks derive from the unpredictability of GETs and are modulated by delivery mode and target cells

With regards to safety in therapy, the genome editing community initially focused on the potential OT activity of GETs <sup>7,9</sup>. However, these events are proving to be relatively rare in comparison with local rearrangements following on-target activity <sup>34-36,39,46</sup>, which are newly recognized and are likely to be studied further. Many questions arise, such as the size of the rearrangements, the frequency of each type of event (for example, larger than designed deletions, inversions, duplications, and combinations of these) and the specific consequences attached to the modification of each targeted locus (for example, potential activation of an oncogene or other pathogenic gene in the vicinity). The question of specificity can also be applied at several levels: do GETs solely cut where expected; and what are the functional consequences of the repairs in each genomic region affected? Answering these questions requires sensitive means of detecting mutagenic events that are themselves still the objects of improvement <sup>89</sup>. These studies are essential to ensure the reproducibility of all research involving GET use. But in the clinic, unlike in biomedical research, only cases where those changes are both functional and pathogenic will represent a safety concern.

The unwanted consequences of using GETs also needs to be assessed in the relevant systems. Studies in human cells will inform on safety in relation to the interaction of GETs with the human genome <sup>7,19-22</sup> and on expected repairs of the genetic interval containing the targeted locus <sup>36</sup>. The choice of *in vitro* model is paramount, as cellular repair systems are lineage-specific <sup>90</sup>. Animal models may not represent human repair systems, but will inform on safety at the level of the whole organism and are also useful for studying the consequences of DNA repair activity. Humanized mouse strains in which the mouse allele is replaced by the full human sequence ally the advantages of working with the relevant target locus in the context of a whole organism<sup>91</sup>. Evidently, different models have different biases; cell culture itself is known to introduce changes that affect genome integrity <sup>92</sup>. Furthermore, the mode of delivery in cell culture is different to that *in vivo*, as it often involves sustained expression of GETs. Conversely, animal models may lack the specific (human) genetic sequences (and potential OT sites) for which the GETs are intended. Full evaluation must include the consideration of safety issues associated with GETs and their mode of delivery. Cell culture and animal models are therefore both complementary and essential, but cannot replace safety trials in patients. Initial attempts to understand unwanted effects of GETs on the genome included whole genome sequencing and capture of GET-related events in cell culture models <sup>7-10,24</sup>. These approaches, although informative, did not identify larger scale changes, such as chromosomal rearrangements and larger deletions. As the research field matures, methods for the detection and characterization of these initially unexpected repair events are being developed and applied in a more systematic fashion, uncovering a hitherto underestimated variability in outcomes. Table 1 summarizes the most relevant techniques employed to analyze the genomic consequences of GET use. In particular, methods for counting the copy number of specific alleles and long-read sequencing have changed our perception of GET activity <sup>34,36,46,93</sup>. Such methods will be instrumental tools for the validation of research models, assessment of GET genotoxicity and definition of DNA mutation signatures associated with risks. Next generation sequencing (NGS)

detects a large panel of single nucleotide polymorphism mutations and small indels in the entire genome. However, unless very large depth of coverage is achieved, short-read NGS does not reliably detect structural variation mutations, and some genomic regions (for example repetitive or structurally challenging sequences) are poorly amplified or aligned. By contrast, linear amplification-mediated high-throughput genome-wide sequencing detects DSBs with high sensitivity by employing a fixed 'bait' DSB to capture them prior to cloning and short read NGS sequencing. This method allows for a nucleotide-level definition of genomic rearrangements without the requirement of pre-defining potential OT sites. Long-read NGS methodologies are also beginning to be employed to analyse the outcome of genome editing, through targeted sequencing, for in-depth analysis of specific loci, or for whole genome sequencing in replacement or in combination with short-read NGS <sup>94</sup>. For all whole genome methodologies, the number of mutation events detected can be high, making it difficult to distinguish between causative and non-essential mutations. Cytogenetic methods <sup>38</sup> and next generation mapping sensitively identifies large genomic variations that can be missed by PCR-based techniques, NGS or chromosomal microarrays <sup>93</sup>. Again, the ability to distinguish between pathogenic structural variants and benign mutations remains challenging.

As new diagnostic tools are developed, new features of GET activity are revealed and no single approach currently encompasses the detection of all possible mutagenic events. Today in the clinic, the DNA mutation signature obtained through the combination of these diagnostic tools generally precludes definition of the risk of toxicity. Predicting what these data mean remains highly speculative but if toxicity arises the data will be essential to define adequate and unacceptable DNA mutation signatures.

Additionally, the impact of genomic alterations will differ according to the targeted cell type. For example, therapies that propose to disrupt integrated HIV sequences by CRISPR/Cas9 <sup>95</sup> are likely to generate multiple genomic rearrangements: as multiple copies of HIV can be integrated into a single cell genome <sup>96</sup>, DNA repair of multiple DSBs could trigger large rearrangements or translocations. Transformation risk is, however,

low for T cells compared to other cell types. By contrast, for cystic fibrosis, after GET-mediated correction of the patient's induced pluripotent stem cells (iPSCs), no significant OT events were detected <sup>97</sup> but the cancer transformation risk of iPSCs is much higher.

In summary, the clinical risk will be defined by a complex combination of factors: the induced genomic variations, the delivery mode of GETs and the cellular context (Figure 1).

### How can we control safety risks?

Three therapeutic pathways have been proposed for GETs in the clinic; *ex vivo* tissue engineering followed by grafting <sup>81</sup>, somatic delivery of GETs <sup>81</sup>, and early embryo genome modification that will be transmitted through the germline <sup>98</sup>. In all three cases, GET design, and in particular the choice of sgRNAs for CRISPR/Cas9-based approaches, is the first issue to consider. Many studies indicate that GET OT activity depends on sgRNA sequence <sup>7,21</sup>; designs should be optimized to minimize the OT activity, in particular with the relevant mode of delivery. On-target mutations following cell genomic repairs will be equally if not more important to assess when designing a GET, as they can involve a large variety of changes including larger-than-expected deletions and chromosomal rearrangements. These issues need to be assessed in the cellular context(s) for which they are intended in therapy, as the way in which targeted cells repair specific DSBs may differ between cell types, cell cycle phase, metabolic status and levels of cell differentiation <sup>90</sup>. Interestingly, some studies propose that not only is the mutational outcome dependent on both the target sequence and cell line, but that the outcome is also partly predictable <sup>99</sup>. Careful validation of the design of GETs to limit the range of, mutations generated at each target is essential to a reduction in risks associated with their use. However, even with the knowledge of the patient's genome sequence and sophisticated prediction software, an exhaustive OT risk profile may not entirely be

defined in preclinical studies or in clinical trials and may require investigation of reactivity of the GETs in the cells of each patient.

Other considerations are more specific to the given mode of GET delivery. If edited cells can be selected *in vitro* prior to grafting or re-implantation, infrequent mutations may represent less of a barrier to GET use. In such cases, if the therapeutic design allows for the selection of clones or pools of cells that only contain an acceptable outcome of genome editing, any unwanted events could then be discarded. Recent studies have reported that GETs induce DNA damage response. Thus, they may carry a risk for cancer due to selection against cells with a functional *P53* but also with *VHL* and *KRAS* mutations<sup>49,50,100</sup>. Quality control of engineered tissue should also address other features related to the use of *in vitro* methods. For example, karyotype and epigenetic changes are common occurrences that are linked to tissue culturing and to methods of transfection<sup>92</sup> and may represent as significant a carcinogenic risk as the use of GETs itself.

Somatic delivery may present different challenges<sup>101</sup>. Following safety issues with viral sequence insertions<sup>72</sup>, current trials are mainly focused on non-integrative approaches<sup>81</sup>. However, even if integration-deficient viruses are used, insertion of viral sequences may occur in time<sup>102</sup>. Critically, adenovirus or AAV-mediated delivery may lead to long-term expression of a targeted mutagenic agent<sup>103</sup> and therefore carries an increased risk of OT events. Strategies may therefore favor transient expression using RNP or mRNA that will reduce the time of exposure to Cas9 nuclease<sup>104</sup>, supported by a viral vector<sup>105</sup> or other modes of delivery, such as liposomes or association to gold particles<sup>106</sup>. Furthermore, the expression itself of nucleases may carry the risk of immune reaction, as shown by the identification of immunogenicity against *Staphylococcus aureus* and *Streptococcus pyogenes* (*Sp*) Cas9 proteins in humans<sup>107,108</sup>. Such issues may be circumvented by the use of alternative nucleases, transient Cas9 expression or the combination of GET with transient immunosuppressant treatment. The frequency of such pre-existing adaptive immunity is not fully understood and may reflect a balance

between the activities of *SpCas9*-reactive regulatory T cells and *SpCas9*-reactive effector T cells<sup>107</sup>.

Genome editing of the early human embryo or gamete is not the subject of current registered trials, but methods applicable to such interventions are being developed<sup>109</sup>. Early attempts to modify human embryos, including unlicensed trials, have encountered the same challenges as those that are experienced when using animal models, such as mosaicism or unpredictability of the repair outcome<sup>98</sup>. Existing methods employed in prenatal diagnostics, such as pre-implantation diagnosis after *in vitro* fertilization, may offer lower risk by selecting offspring free of genetic diseases. However, these techniques are not applicable to all families (for example, in cases when no unaffected embryo is available). Such issues continue to be subjects of ethical debate on germline modification in humans<sup>110</sup>.

Potentially applicable to all three routes of delivery is the ongoing development of new GETs. A wide variety of strategies have been tried, including the engineering of nucleases with higher specificity<sup>111,112</sup>, the coupling of Cas9 fusions with specific protein domains to enhance the frequency of DSB repair by homology directed repair (see<sup>113</sup> for review), and the abolition of all nuclease activity with the coupling of another effector, such as modules that edit DNA base identity<sup>114</sup>. The latter seems particularly attractive as many safety issues stem from our inability to direct the mode of DSB repair that follows GET activity. However, current versions of these base-editing tools do not yet allow the precise prediction of the outcome of their use and while point mutations other than C → T and A → G are not feasible to date<sup>114</sup>, there may be immediate applications aimed at creating targeted gene knockouts and new generations of base editors are being developed<sup>115</sup>. Nickase variants of GETs may also represent possible safety improvements<sup>116</sup>, but the molecular mechanisms that are involved when nickases are used for genome editing remain poorly understood, and all safety caveats associated with the use of nucleases may also apply<sup>42</sup>. A most recent addition to the GET set is a system with two nickases coupled to a reverse transcription activity to be used in conjunction with hybrid



guides that also contain a repair template sequence for genome modification by prime editing <sup>117</sup>. Appraisal of the applicability and reliability of such advanced strategies will await extensive trials in both the research and pre-clinical settings. Looking further ahead, methods to transiently direct DSB repair cell mechanisms to yield the desired outcome would represent an attractive solution that so far has eluded the field <sup>118</sup>.

## Conclusion

In spite of their initial promise, GETs have not yet yielded a flawless capacity to modify genomic sequences specifically and predictably, either in research or in the clinic. Although their use is highly efficient, the outcomes can be unpredictable. In the research environment, it is important that the experimental design takes into account the possibility of unwanted DNA repair outcomes, excludes undesired events by validation of edited models, and employs appropriate controls to ensure research reproducibility. In the clinic, there are likely to be ongoing improvements to genome editing efficiency, delivery systems, and techniques to map on- and off-target effects. The first clinical applications are already underway in areas of unmet need, such as hematological malignancy, using *ex-vivo* modified somatic and differentiated T cells. Applications using *ex-vivo* CRISPR/Cas9 edited HSCs for hemaglobinopathies are imminent, and patients will be subjected to close long-term monitoring, as are patients who receive *in vivo* therapy for certain life-threatening metabolic conditions. Careful monitoring and in-depth consideration, including deep molecular interrogation of any adverse effects, will be the key to successful exploitation of these tools.

## Abbreviations

AAV, adeno-associated virus; CCR5, C-C chemokine receptor type 5; CRISPR, clustered regularly interspaced short palindromic repeats; DNA, deoxyribonucleic acid; DSB, double stranded break; FISH, fluorescence in situ hybridization; GET, genome editing tool; HAART, highly active antiretroviral therapy; HIV, human immunodeficiency virus; HLA, human leukocyte antigen ; HPV, human papillomavirus; HSC, hematopoietic stem cells; iPSC, induced pluripotent stem cells; NGS, next generation sequencing; OT, off-target; PCR, polymerase chain reaction; PD-1, programmed cell death protein 1; RNA, ribonucleic acid; SCID, severe combined immunodeficiency; sgRNA, single guide RNA; SNP, single nucleotide polymorphisms; *Sp*, *Streptococcus pyogenes*; TALEN, transcription activator-like effector nuclease; TCR, T-cell receptor; ZFN, zinc finger nucleases.

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## Author contributions

All authors have contributed to the writing of the manuscript. All authors read and approved the final manuscript.

## Disclosure/Conflict of Interest

The authors have no conflict of interest to disclose.

## References

1. Porteus, MH (2019). A New Class of Medicines through DNA Editing. *N. Engl. J. Med.* **380**: 947–959.
2. Pickar-Oliver, A and Gersbach, CA (2019). The next generation of CRISPR–Cas technologies and applications. *Nat. Rev. Mol. Cell Biol.* **20**: 490–507.
3. Mullard, A (2019). First in vivo CRISPR candidate enters the clinic. *Nat. Rev. Drug Discov.* **18**: 656–656.
4. Ledford, H (2020). Quest to use CRISPR against disease gains ground. *Nature* **577**: 156–156.
5. Hamilton, JR and Doudna, JA (2020). Knocking out barriers to engineered cell activity. *Science*: eaba9844doi:10.1126/science.aba9844.
6. Ledford, H. CRISPR treatment inserted directly into the body for first time. *Nature*doi:10.1038/d41586-020-00655-8.
7. Fu, Y, Foden, JA, Khayter, C, Maeder, ML, Reyon, D, Joung, JK, *et al.* (2013). High-frequency off-target mutagenesis induced by CRISPR-Cas nucleases in human cells. *Nat. Biotechnol.* **31**: 822–826.
8. Pattanayak, V, Lin, S, Guilinger, JP, Ma, E, Doudna, JA and Liu, DR (2013). High-throughput profiling of off-target DNA cleavage reveals RNA-programmed Cas9 nuclease specificity. *Nat. Biotechnol.* **31**: 839–843.
9. Pattanayak, V, Ramirez, CL, Joung, JK and Liu, DR (2011). Revealing off-target cleavage specificities of zinc-finger nucleases by in vitro selection. *Nat. Methods* **8**: 765–770.
10. Tsai, SQ, Zheng, Z, Nguyen, NT, Liebers, M, Topkar, VV, Thapar, V, *et al.* (2015). GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. *Nat. Biotechnol.* **33**: 187–197.
11. Iyer, V, Boroviak, K, Thomas, M, Doe, B, Riva, L, Ryder, E, *et al.* (2018). No unexpected CRISPR-Cas9 off-target activity revealed by trio sequencing of gene-edited mice. *PLoS Genet.* **14**: e1007503.
12. Nakajima, K, Kazuno, A-A, Kelsoe, J, Nakanishi, M, Takumi, T and Kato, T (2016). Exome sequencing in the knockin mice generated using the CRISPR/Cas system. *Sci. Rep.* **6**: 34703.
13. Iyer, V, Shen, B, Zhang, W, Hodgkins, A, Keane, T, Huang, X, *et al.* (2015). Off-target mutations are rare in Cas9-modified mice. *Nat. Methods* **12**: 479.
14. Nekrasov, V, Wang, C, Win, J, Lanz, C, Weigel, D and Kamoun, S (2017). Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. *Sci. Rep.* **7**: 482.
15. Tang, X, Liu, G, Zhou, J, Ren, Q, You, Q, Tian, L, *et al.* (2018). A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 (Cas12a) nucleases in rice. *Genome Biol.* **19**: 84.
16. Zhang, H, Zhang, J, Wei, P, Zhang, B, Gou, F, Feng, Z, *et al.* (2014). The CRISPR/Cas9 system produces specific and homozygous targeted gene editing in rice in one generation. *Plant Biotechnol. J.* **12**: 797–807.
17. Feng, Z, Mao, Y, Xu, N, Zhang, B, Wei, P, Yang, D-L, *et al.* (2014). Multigeneration analysis reveals the inheritance, specificity, and patterns of CRISPR/Cas-induced gene modifications in Arabidopsis. *Proc. Natl. Acad. Sci. U. S. A.* **111**: 4632–4637.
18. Hruscha, A, Krawitz, P, Rechenberg, A, Heinrich, V, Hecht, J, Haass, C, *et al.* (2013). Efficient CRISPR/Cas9 genome editing with low off-target effects in zebrafish. *Dev. Camb. Engl.* **140**: 4982–4987.
19. Kim, D, Bae, S, Park, J, Kim, E, Kim, S, Yu, HR, *et al.* (2015). Digenome-seq: genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. *Nat. Methods* **12**: 237–243, 1 p following 243.
20. Smith, C, Gore, A, Yan, W, Abalde-Atristain, L, Li, Z, He, C, *et al.* (2014). Whole-genome sequencing analysis reveals high specificity of CRISPR/Cas9 and TALEN-based genome editing in human iPSCs. *Cell Stem Cell* **15**: 12–13.

21. Veres, A, Gosis, BS, Ding, Q, Collins, R, Ragavendran, A, Brand, H, *et al.* (2014). Low incidence of off-target mutations in individual CRISPR-Cas9 and TALEN targeted human stem cell clones detected by whole-genome sequencing. *Cell Stem Cell* **15**: 27–30.
22. Knipping, F, Osborn, MJ, Petri, K, Tolar, J, Glimm, H, von Kalle, C, *et al.* (2017). Genome-wide Specificity of Highly Efficient TALENs and CRISPR/Cas9 for T Cell Receptor Modification. *Mol. Ther. Methods Clin. Dev.* **4**: 213–224.
23. Osborn, MJ, Webber, BR, Knipping, F, Lonetree, C, Tennis, N, DeFeo, AP, *et al.* (2016). Evaluation of TCR Gene Editing Achieved by TALENs, CRISPR/Cas9, and megaTAL Nucleases. *Mol. Ther. J. Am. Soc. Gene Ther.* **24**: 570–581.
24. Cho, SW, Kim, S, Kim, Y, Kweon, J, Kim, HS, Bae, S, *et al.* (2014). Analysis of off-target effects of CRISPR/Cas-derived RNA-guided endonucleases and nickases. *Genome Res.* **24**: 132–141.
25. Schaefer, KA, Wu, W-H, Colgan, DF, Tsang, SH, Bassuk, AG and Mahajan, VB (2017). Unexpected mutations after CRISPR-Cas9 editing in vivo. *Nat. Methods* **14**: 547–548.
26. Wang, X, Wang, Y, Wu, X, Wang, J, Wang, Y, Qiu, Z, *et al.* (2015). Unbiased detection of off-target cleavage by CRISPR-Cas9 and TALENs using integrase-defective lentiviral vectors. *Nat. Biotechnol.* **33**: 175–178.
27. Kim, S-T, Park, J, Kim, D, Kim, K, Bae, S, Schlesner, M, *et al.* (2018). Response to “Unexpected mutations after CRISPR–Cas9 editing in vivo”. *Nat. Methods* **15**: 239–240.
28. Lareau, CA, Clement, K, Hsu, JY, Pattanayak, V, Joung, JK, Aryee, MJ, *et al.* (2018). Response to “Unexpected mutations after CRISPR–Cas9 editing in vivo”. *Nat. Methods* **15**: 238.
29. Lescarbeau, RM, Murray, B, Barnes, TM and Bermingham, N (2018). Response to “Unexpected mutations after CRISPR–Cas9 editing in vivo”. *Nat. Methods* **15**: 237–237.
30. Nutter, LMJ, Heaney, JD, Lloyd, KCK, Murray, SA, Seavitt, JR, Skarnes, WC, *et al.* (2018). Response to “Unexpected mutations after CRISPR–Cas9 editing in vivo”. *Nat. Methods* **15**: 235–236.
31. Wilson, CJ, Fennell, T, Bothmer, A, Maeder, ML, Reyon, D, Cotta-Ramusino, C, *et al.* (2018). Response to “Unexpected mutations after CRISPR–Cas9 editing in vivo”. *Nat. Methods* **15**: 236–237.
32. Lynch, M (2010). Evolution of the mutation rate. *Trends Genet. TIG* **26**: 345–352.
33. Choi, PS and Meyerson, M (2014). Targeted genomic rearrangements using CRISPR/Cas technology. *Nat. Commun.* **5**: 3728.
34. Birling, M-C, Schaeffer, L, André, P, Lindner, L, Maréchal, D, Ayadi, A, *et al.* (2017). Efficient and rapid generation of large genomic variants in rats and mice using CRISMERE. *Sci. Rep.* **7**: 43331.
35. Jiang, J, Zhang, L, Zhou, X, Chen, X, Huang, G, Li, F, *et al.* (2016). Induction of site-specific chromosomal translocations in embryonic stem cells by CRISPR/Cas9. *Sci. Rep.* **6**: 21918.
36. Kosicki, M, Tomberg, K and Bradley, A (2018). Repair of double-strand breaks induced by CRISPR-Cas9 leads to large deletions and complex rearrangements. *Nat. Biotechnol.* doi:10.1038/nbt.4192.
37. Kraft, K, Geuer, S, Will, AJ, Chan, WL, Paliou, C, Borschiwer, M, *et al.* (2015). Deletions, Inversions, Duplications: Engineering of Structural Variants using CRISPR/Cas in Mice. *Cell Rep.* **10**: 833–839.
38. Rayner, E, Durin, M-A, Thomas, R, Moralli, D, O’Cathail, SM, Tomlinson, I, *et al.* (2019). CRISPR-Cas9 Causes Chromosomal Instability and Rearrangements in Cancer Cell Lines, Detectable by Cytogenetic Methods. *CRISPR J.* **2**: 406–416.
39. Shin, HY, Wang, C, Lee, HK, Yoo, KH, Zeng, X, Kuhns, T, *et al.* (2017). CRISPR/Cas9 targeting events cause complex deletions and insertions at 17 sites in the mouse genome. *Nat. Commun.* **8**: 15464.
40. Lee, HJ, Kweon, J, Kim, E, Kim, S and Kim, J-S (2012). Targeted chromosomal duplications and inversions in the human genome using zinc finger nucleases. *Genome Res.* **22**: 539–548.
41. Ono, R, Ishii, M, Fujihara, Y, Kitazawa, M, Usami, T, Kaneko-Ishino, T, *et al.* (2015). Double strand break repair by capture of retrotransposon sequences and reverse-transcribed spliced mRNA sequences in mouse zygotes. *Sci. Rep.* **5**: 12281.

42. Owens, DDG, Caulder, A, Frontera, V, Harman, JR, Allan, AJ, Bucakci, A, *et al.* (2019). Microhomologies are prevalent at Cas9-induced larger deletions. *Nucleic Acids Res.*doi:10.1093/nar/gkz459.
43. Simeonov, DR, Brandt, AJ, Chan, AY, Cortez, JT, Li, Z, Woo, JM, *et al.* (2019). A large CRISPR-induced bystander mutation causes immune dysregulation. *Commun. Biol.* **2**: 70.
44. Low, BE, Krebs, MP, Joung, JK, Tsai, SQ, Nishina, PM and Wiles, MV (2014). Correction of the *Crb1rd8* allele and retinal phenotype in C57BL/6N mice via TALEN-mediated homology-directed repair. *Invest. Ophthalmol. Vis. Sci.* **55**: 387–395.
45. Renaud, J-B, Boix, C, Charpentier, M, De Cian, A, Cochenec, J, Duvernois-Berthet, E, *et al.* (2016). Improved Genome Editing Efficiency and Flexibility Using Modified Oligonucleotides with TALEN and CRISPR-Cas9 Nucleases. *Cell Rep.* **14**: 2263–2272.
46. Codner, GF, Mianné, J, Caulder, A, Loeffler, J, Fell, R, King, R, *et al.* (2018). Application of long single-stranded DNA donors in genome editing: generation and validation of mouse mutants. *BMC Biol.* **16**: 70.
47. Canaj, H, Hussmann, JA, Li, H, Beckman, KA, Goodrich, L, Cho, NH, *et al.* (2019). Deep profiling reveals substantial heterogeneity of integration outcomes in CRISPR knock-in experiments. *bioRxiv*: 841098doi:10.1101/841098.
48. Goodarzi, AA and Jeggo, PA (2013). The repair and signaling responses to DNA double-strand breaks. *Adv. Genet.* **82**: 1–45.
49. Haapaniemi, E, Botla, S, Persson, J, Schmierer, B and Taipale, J (2018). CRISPR-Cas9 genome editing induces a p53-mediated DNA damage response. *Nat. Med.*doi:10.1038/s41591-018-0049-z.
50. Ihry, RJ, Worringer, KA, Salick, MR, Frias, E, Ho, D, Theriault, K, *et al.* (2018). p53 inhibits CRISPR-Cas9 engineering in human pluripotent stem cells. *Nat. Med.*doi:10.1038/s41591-018-0050-6.
51. Mehta, A and Haber, JE (2014). Sources of DNA double-strand breaks and models of recombinational DNA repair. *Cold Spring Harb. Perspect. Biol.* **6**: a016428.
52. Sallmyr, A and Tomkinson, AE (2018). Repair of DNA double-strand breaks by mammalian alternative end-joining pathways. *J. Biol. Chem.* **293**: 10536–10546.
53. Sinha, S, Guerra, KB, Cheng, K, Leiserson, MD, Wilson, DM, Ryan, BM, *et al.* (2019). Integrated computational and experimental identification of p53, KRAS and VHL mutant selection associated with CRISPR-Cas9 editing. *bioRxiv*doi:10.1101/407767.
54. Justice, MJ and Dhillon, P (2016). Using the mouse to model human disease: increasing validity and reproducibility. *Dis. Model. Mech.* **9**: 101–103.
55. Wang, H, Yang, H, Shivalila, CS, Dawlaty, MM, Cheng, AW, Zhang, F, *et al.* (2013). One-step generation of mice carrying mutations in multiple genes by CRISPR/Cas-mediated genome engineering. *Cell* **153**: 910–918.
56. Teboul, L, Murray, SA and Nolan, PM (2017). Phenotyping first-generation genome editing mutants: a new standard? *Mamm. Genome Off. J. Int. Mamm. Genome Soc.* **28**: 377–382.
57. Nelson, CE, Wu, Y, Gemberling, MP, Oliver, ML, Waller, MA, Bohning, JD, *et al.* (2019). Long-term evaluation of AAV-CRISPR genome editing for Duchenne muscular dystrophy. *Nat. Med.* **25**: 427–432.
58. Tebas, P, Stein, D, Tang, WW, Frank, I, Wang, SQ, Lee, G, *et al.* (2014). Gene editing of CCR5 in autologous CD4 T cells of persons infected with HIV. *N. Engl. J. Med.* **370**: 901–910.
59. Kaiser, J (2017). A human has been injected with gene-editing tools to cure his disabling disease. Here's what you need to know. *Sciencedoi*:10.1126/science.aar5098.
60. Kaiser, J (2018). New gene-editing treatment might help treat a rare disorder, hints first human test. *Sciencedoi*:10.1126/science.aav3226.
61. Qasim, W, Zhan, H, Samarasinghe, S, Adams, S, Amrolia, P, Stafford, S, *et al.* (2017). Molecular remission of infant B-ALL after infusion of universal TALEN gene-edited CAR T cells. *Sci. Transl. Med.* **9**.
62. Reardon, S (2015). Leukaemia success heralds wave of gene-editing therapies. *Nature* **527**: 146–147.

63. Benjamin, R, Graham, C, Yallop, D, Jozwik, A, Ciocarlie, O, Jain, N, *et al.* (2018). Preliminary Data on Safety, Cellular Kinetics and Anti-Leukemic Activity of UCART19, an Allogeneic Anti-CD19 CAR T-Cell Product, in a Pool of Adult and Pediatric Patients with High-Risk CD19+ Relapsed/Refractory B-Cell Acute Lymphoblastic Leukemiaat <<https://ash.confex.com/ash/2018/webprogram/Paper111356.html>>.
64. Poirot, L, Philip, B, Schiffer-Mannioui, C, Le Clerre, D, Chion-Sotinel, I, Derniame, S, *et al.* (2015). Multiplex Genome-Edited T-cell Manufacturing Platform for ‘Off-the-Shelf’ Adoptive T-cell Immunotherapies. *Cancer Res.* **75**: 3853–3864.
65. Normile, D (2017). China sprints ahead in CRISPR therapy race. *Science* **358**: 20–21.
66. Stadtmauer, EA, Fraietta, JA, Davis, MM, Cohen, AD, Weber, KL, Lancaster, E, *et al.* (2020). CRISPR-engineered T cells in patients with refractory cancer. *Science*: eaba7365doi:10.1126/science.aba7365.
67. Xu, L, Wang, J, Liu, Y, Xie, L, Su, B, Mou, D, *et al.* (2019). CRISPR-Edited Stem Cells in a Patient with HIV and Acute Lymphocytic Leukemia. *N. Engl. J. Med.* **381**: 1240–1247.
68. Reardon, S (2019). First CRISPR editing trial results assuage safety concerns. *Nat. Med.*doi:10.1038/d41591-019-00019-4.
69. The Lancet Haematology (2019). CRISPR-Cas9 gene editing for patients with haemoglobinopathies. *Lancet Haematol.* **6**: e438.
70. Cyranoski, D and Ledford, H (2018). Genome-edited baby claim provokes international outcry. *Nature* **563**: 607–608.
71. Wood, ME, Vogel, V, Ng, A, Foxhall, L, Goodwin, P and Travis, LB (2012). Second malignant neoplasms: assessment and strategies for risk reduction. *J. Clin. Oncol. Off. J. Am. Soc. Clin. Oncol.* **30**: 3734–3745.
72. Hacein-Bey-Abina, S, Von Kalle, C, Schmidt, M, McCormack, MP, Wulffraat, N, Leboulch, P, *et al.* (2003). LMO2-associated clonal T cell proliferation in two patients after gene therapy for SCID-X1. *Science* **302**: 415–419.
73. Ott, MG, Schmidt, M, Schwarzwaelder, K, Stein, S, Siler, U, Koehl, U, *et al.* (2006). Correction of X-linked chronic granulomatous disease by gene therapy, augmented by insertional activation of MDS1-EVI1, PRDM16 or SETBP1. *Nat. Med.* **12**: 401–409.
74. Braun, CJ, Boztug, K, Paruzynski, A, Witzel, M, Schwarzer, A, Rothe, M, *et al.* (2014). Gene therapy for Wiskott-Aldrich syndrome--long-term efficacy and genotoxicity. *Sci. Transl. Med.* **6**: 227ra33.
75. Montini, E, Cesana, D, Schmidt, M, Sanvito, F, Bartholomae, CC, Ranzani, M, *et al.* (2009). The genotoxic potential of retroviral vectors is strongly modulated by vector design and integration site selection in a mouse model of HSC gene therapy. *J. Clin. Invest.* **119**: 964–975.
76. Hacein-Bey-Abina, S, Pai, S-Y, Gaspar, HB, Armant, M, Berry, CC, Blanche, S, *et al.* (2014). A Modified  $\gamma$ -Retrovirus Vector for X-Linked Severe Combined Immunodeficiency. *N. Engl. J. Med.* **371**: 1407–1417.
77. Aiuti, A, Cattaneo, F, Galimberti, S, Benninghoff, U, Cassani, B, Callegaro, L, *et al.* (2009). Gene therapy for immunodeficiency due to adenosine deaminase deficiency. *N. Engl. J. Med.* **360**: 447–458.
78. Qasim, W, Gaspar, HB and Thrasher, AJ (2009). Progress and prospects: gene therapy for inherited immunodeficiencies. *Gene Ther.* **16**: 1285–1291.
79. Haeussler, M, Schönig, K, Eckert, H, Eschstruth, A, Mianné, J, Renaud, J-B, *et al.* (2016). Evaluation of off-target and on-target scoring algorithms and integration into the guide RNA selection tool CRISPOR. *Genome Biol.* **17**.
80. Teboul, L and Greenfield, A (2018). CRISPR-Cas9-Mediated Mutagenesis: Mind the Gap? *CRISPR J.* **1**: 263–264.
81. Shim, G, Kim, D, Park, GT, Jin, H, Suh, S-K and Oh, Y-K (2017). Therapeutic gene editing: delivery and regulatory perspectives. *Acta Pharmacol. Sin.* **38**: 738–753.
82. Lino, CA, Harper, JC, Carney, JP and Timlin, JA (2018). Delivering CRISPR: a review of the challenges and approaches. *Drug Deliv.* **25**: 1234–1257.

83. Hacein-Bey-Abina, S, von Kalle, C, Schmidt, M, Le Deist, F, Wulffraat, N, McIntyre, E, *et al.* (2003). A serious adverse event after successful gene therapy for X-linked severe combined immunodeficiency. *N. Engl. J. Med.* **348**: 255–256.
84. Thomas, CE, Ehrhardt, A and Kay, MA (2003). Progress and problems with the use of viral vectors for gene therapy. *Nat. Rev. Genet.* **4**: 346–358.
85. Mann, CJ, Anguela, XM, Montané, J, Obach, M, Roca, C, Ruzo, A, *et al.* (2012). Molecular signature of the immune and tissue response to non-coding plasmid DNA in skeletal muscle after electrotransfer. *Gene Ther.* **19**: 1177–1186.
86. Wong, TWY and Cohn, RD (2017). Therapeutic Applications of CRISPR/Cas for Duchenne Muscular Dystrophy. *Curr. Gene Ther.* **17**: 301–308.
87. Mollanoori, H, Rahmati, Y, Hassani, B, Havasi Mehr, M and Teimourian, S (2020). Promising therapeutic approaches using CRISPR/Cas9 genome editing technology in the treatment of Duchenne muscular dystrophy. *Genes Dis.* doi:10.1016/j.gendis.2019.12.007.
88. Huang, Z, Tomitaka, A, Raymond, A and Nair, M (2017). Current application of CRISPR/Cas9 gene-editing technique to eradication of HIV/AIDS. *Gene Ther.* **24**: 377.
89. Levy, SE and Myers, RM (2016). Advancements in Next-Generation Sequencing. *Annu. Rev. Genomics Hum. Genet.* **17**: 95–115.
90. Shrivastav, M, De Haro, LP and Nickoloff, JA (2007). Regulation of DNA double-strand break repair pathway choice. *Cell Res.* **18**: 134.
91. Aartsma-Rus, A and van Putten, M (2019). The use of genetically humanized animal models for personalized medicine approaches. *Dis. Model. Mech.* **13**: dmm041673.
92. Assou, S, Bouckenheimer, J and De Vos, J (2018). Concise Review: Assessing the Genome Integrity of Human Induced Pluripotent Stem Cells: What Quality Control Metrics? *Stem Cells Dayt. Ohio* **36**: 814–821.
93. Barseghyan, H, Tang, W, Wang, RT, Almalvez, M, Segura, E, Bramble, MS, *et al.* (2017). Next-generation mapping: a novel approach for detection of pathogenic structural variants with a potential utility in clinical diagnosis. *Genome Med.* **9**.
94. Nakano, K, Shiroma, A, Shimoji, M, Tamotsu, H, Ashimine, N, Ohki, S, *et al.* (2017). Advantages of genome sequencing by long-read sequencer using SMRT technology in medical area. *Hum. Cell* **30**: 149–161.
95. Ebina, H, Misawa, N, Kanemura, Y and Koyanagi, Y (2013). Harnessing the CRISPR/Cas9 system to disrupt latent HIV-1 provirus. *Sci. Rep.* **3**: 2510.
96. Del Portillo, A, Tripodi, J, Najfeld, V, Wodarz, D, Levy, DN and Chen, BK (2011). Multiploid Inheritance of HIV-1 during Cell-to-Cell Infection. *J. Virol.* **85**: 7169–7176.
97. Crane, AM, Kramer, P, Bui, JH, Chung, WJ, Li, XS, Gonzalez-Garay, ML, *et al.* (2015). Targeted Correction and Restored Function of the CFTR Gene in Cystic Fibrosis Induced Pluripotent Stem Cells. *Stem Cell Rep.* **4**: 569–577.
98. Liang, P, Xu, Y, Zhang, X, Ding, C, Huang, R, Zhang, Z, *et al.* (2015). CRISPR/Cas9-mediated gene editing in human triploid zygotes. *Protein Cell* **6**: 363–372.
99. Allen, F, Crepaldi, L, Alsinet, C, Strong, AJ, Kleshchevnikov, V, De Angeli, P, *et al.* (2018). Predicting the mutations generated by repair of Cas9-induced double-strand breaks. *Nat. Biotechnol.* doi:10.1038/nbt.4317.
100. Sinha, S, Cheng, K, Leiserson, MD, Wilson, DM, Ryan, BM, Lee, JS, *et al.* (2018). A systematic genome-wide mapping of the oncogenic risks associated with CRISPR-Cas9 editing. *bioRxiv* doi:10.1101/407767.
101. Tong, S, Moyo, B, Lee, CM, Leong, K and Bao, G (2019). Engineered materials for in vivo delivery of genome-editing machinery. *Nat. Rev. Mater.* **4**: 726–737.
102. Stephen, SL, Montini, E, Sivanandam, VG, Al-Dhalimy, M, Kestler, HA, Finegold, M, *et al.* (2010). Chromosomal integration of adenoviral vector DNA in vivo. *J. Virol.* **84**: 9987–9994.
103. Schnepf, BC, Chulay, JD, Ye, G-J, Flotte, TR, Trapnell, BC and Johnson, PR (2016). Recombinant Adeno-Associated Virus Vector Genomes Take the Form of Long-Lived, Transcriptionally Competent Episomes in Human Muscle. *Hum. Gene Ther.* **27**: 32–42.

104. Wilbie, D, Walther, J and Mastrobattista, E (2019). Delivery Aspects of CRISPR/Cas for in Vivo Genome Editing. *Acc. Chem. Res.* **52**: 1555–1564.
105. Prel, A, Caval, V, Gayon, R, Ravassard, P, Duthoit, C, Payen, E, *et al.* (2015). Highly efficient in vitro and in vivo delivery of functional RNAs using new versatile MS2-chimeric retrovirus-like particles. *Mol. Ther. Methods Clin. Dev.* **2**: 15039.
106. Wang, M, Glass, ZA and Xu, Q (2016). Non-viral delivery of genome-editing nucleases for gene therapy. *Gene Ther.* **24**: 144.
107. Wagner, DL, Amini, L, Wendering, DJ, Burkhardt, L-M, Akyüz, L, Reinke, P, *et al.* (2019). High prevalence of Streptococcus pyogenes Cas9-reactive T cells within the adult human population. *Nat. Med.* **25**: 242–248.
108. Charlesworth, CT, Deshpande, PS, Dever, DP, Camarena, J, Lemgart, VT, Cromer, MK, *et al.* (2019). Identification of preexisting adaptive immunity to Cas9 proteins in humans. *Nat. Med.* **25**: 249–254.
109. Fogarty, NME, McCarthy, A, Snijders, KE, Powell, BE, Kubikova, N, Blakeley, P, *et al.* (2017). Genome editing reveals a role for OCT4 in human embryogenesis. *Nature* **550**: 67.
110. Jasanoff, S and Hurlbut, JB (2018). A global observatory for gene editing. *Nature* **555**: 435–437.
111. Vakulskas, CA, Dever, DP, Rettig, GR, Turk, R, Jacobi, AM, Collingwood, MA, *et al.* (2018). A high-fidelity Cas9 mutant delivered as a ribonucleoprotein complex enables efficient gene editing in human hematopoietic stem and progenitor cells. *Nat. Med.* **24**: 1216–1224.
112. Casini, A, Olivieri, M, Petris, G, Montagna, C, Reginato, G, Maule, G, *et al.* (2018). A highly specific SpCas9 variant is identified by in vivo screening in yeast. *Nat. Biotechnol.* **36**: 265–271.
113. Devkota, S (2018). The road less traveled: strategies to enhance the frequency of homology-directed repair (HDR) for increased efficiency of CRISPR/Cas-mediated transgenesis. *BMB Rep.* **51**: 437–443.
114. Eid, A, Alshareef, S and Mahfouz, MM (2018). CRISPR base editors: genome editing without double-stranded breaks. *Biochem. J.* **475**: 1955–1964.
115. Doman, JL, Raguram, A, Newby, GA and Liu, DR (2020). Evaluation and minimization of Cas9-independent off-target DNA editing by cytosine base editors. *Nat. Biotechnol.* doi:10.1038/s41587-020-0414-6.
116. Ran, FA, Hsu, PD, Lin, C-Y, Gootenberg, JS, Konermann, S, Trevino, AE, *et al.* (2013). Double nicking by RNA-guided CRISPR Cas9 for enhanced genome editing specificity. *Cell* **154**: 1380–1389.
117. Anzalone, AV, Randolph, PB, Davis, JR, Sousa, AA, Koblan, LW, Levy, JM, *et al.* (2019). Search-and-replace genome editing without double-strand breaks or donor DNA. *Nature* doi:10.1038/s41586-019-1711-4.
118. Danner, E, Bashir, S, Yumlu, S, Wurst, W, Wefers, B and Kühn, R (2017). Control of gene editing by manipulation of DNA repair mechanisms. *Mamm. Genome Off. J. Int. Mamm. Genome Soc.* **28**: 262–274.
119. Frock, RL, Hu, J, Meyers, RM, Ho, Y-J, Kii, E and Alt, FW (2015). Genome-wide detection of DNA double-stranded breaks induced by engineered nucleases. *Nat. Biotechnol.* **33**: 179–186.
120. The Wellcome Trust Case Control Consortium, Conrad, DF, Pinto, D, Redon, R, Feuk, L, Gokcumen, O, *et al.* (2010). Origins and functional impact of copy number variation in the human genome. *Nature* **464**: 704–712.



## Figures legend

Figure 1: Balancing benefits and risks of use of GETs in the clinic.

Each clinical path (cell therapy, somatic therapy or early embryo treatment) carries its own as well as common risk factors. The ratio of benefit to risk of new therapies needs to be individually evaluated for each disease in combination with each therapeutic design.

## Tables

<b>Technique</b>	<b>Advantages</b>	<b>Disadvantages</b>	<b>Reference</b>
Droplet digital PCR	Detection of deletion or duplication on any selected sequence	Only a few selected regions can be checked; for example, potential oncogene or other gene pathogenic in the GET target vicinity	34,46
Short read whole genome NGS	Detection of SNP and small indel mutations in the entire genome, no required OT prediction	Large rearrangements not seen	11
Long read whole genome NGS	More accurate contig generation	Error rate for some instruments	94
Linear amplification-mediated high-throughput genome-wide translocation sequencing	Detection of OT nuclease activity, higher sensitivity, no required OT prediction	Large number of events must be analysed for complete inventory of OT effect	119
Targeted long read sequencing (Nanopore or PacBio)	Precise detection of rearrangement in the vicinity of the target region, high sensitivity	Rearrangements greater than a few kb may not be detected	36,46,47
Chromosomal microarrays	Detection of structural variant	Not all structural variations will be detected. No inversion can be detected by this method	120
FISH	Detection of chromosomal rearrangements	Large rearrangements only are detected	38
Next generation mapping (i.e. Bionano Genomics and genomic vision technologies)	Detection of structural variant	Access to technology and cost for next generation mapping. As Fiber-FISH is based on using probes	93

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and molecular painting  
(Fiber-FISH)

it cannot detect variation  
in the whole genome

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Table 1: Examples of techniques for analyzing genomic consequences of GETs activity.

In all instances appropriate controls are required to differentiate genome editing activity from naturally occurring sequence changes. A full characterisation of genome editing impact requires the implementation of complementary methods. FISH, fluorescence in situ hybridization; GET, genome editing tool; PCR, polymerase chain reaction; SNP, single nucleotide polymorphism

Box 1: Currently recognized risks of using nucleases for GET - key messages

- GETs fit the definition of 'targeted mutagens', as agents that increase the frequency or extent of mutation at a given locus.
- With an experimental design that favours GET transient expression, the frequency of OT mutation is likely to be lower than the natural occurrence of genetic drift for any given generation.
- GET-associated safety risks are also on-target mutations that are the consequences of unwanted DSB repair mechanisms.
- Each GET is different, with its own efficiency and target specificity compared to other GETs.
- Experimental models produced with GETs require extensive molecular validation to ensure research reproducibility.
- The use of GETs as therapeutic agents is associated with three main risk factors; those directly associated with DNA cutting and the resulting repair events, those associated with the delivery means, and those attributable to the biological context in which GETs are employed (that is, which organ systems or cell types are involved).
- GETs need to be assessed in the cellular context(s) for which they are intended in therapy, as the mechanism by which targeted cells repair specific DSBs may differ between cell types, cell cycle phase, metabolic status and level of differentiation.

DNA, deoxyribonucleic acid; DSB, double stranded break; GET, genome editing tools; OT, off-target

## BENEFITS

### Cure + Disease Prevention

(rare diseases, infection,  
cancer and others)

## RISKS

### Cell therapy

Impact on genome of

- Cell culture
- Cell transduction method

Cells removed  
from patient

Cells are modified  
using GETs  
(transient  
expression)

Cells are screened for  
unwanted mutations

GETs viral  
delivery



liposome



gold particle  
GETs non-viral  
delivery

### Somatic therapy

- No means of discarding unwanted events
- Impact of transduction method
- Long-term or high nuclease expression
- Vector toxicity
- Immunogenicity

### Early embryo treatment

- Physical disruption of genetic material
- Disruption of development and health
- Ethical/societal challenge

### Common to all therapeutic approaches

- GETs non-specific cuttings (off-targets)
- Uncontrolled cell repair system resulting in deleterious genomic alterations on target
- Influence of type/degree of differentiation of altered cells
- Pathogenicity of genomic changes to be defined in each case

The benefit to risk balance needs to be evaluated not only for each disease but also **for each GET and delivery mode.**

## Balancing benefits and risks of the use of GETs in the clinic:

Each clinical path (cell therapy, somatic therapy or early embryo treatment) carries its own as well as common risk factors. The ratio of benefit to risk of new therapies needs to be individually evaluated for each disease in combination with each therapeutic design.

