

Crispant analysis in zebrafish as a tool for rapid functional screening of disease-causing genes for bone fragility

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The paper presents a streamlined new approach for functional validation of genes known to underlie fragile bone disorders in a relatively high throughput, using CRISPR-mediated knockouts and a number of phenotypic assessments in zebrafish. **Convincing** data demonstrate the feasibility and validity of this approach, which presents an **important** tool for rapid functional validation of candidate gene(s) associated with heritable bone diseases identified from genetic studies.

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Abstract

Heritable Fragile Bone Disorders (FBDs) encompass a spectrum of conditions, from widespread multifactorial to rare monogenic diseases, all characterized by an elevated risk of fractures. The process of validating causative genes and elucidating their pathogenic mechanisms remains a daunting and resource-intensive task. In this study, we evaluated the feasibility of a semi-high throughput zebrafish screening platform for rapid validation and *in vivo* functional testing and validation of candidate disease-causing genes for a wide range of heritable FBDs. Six genes associated with severe recessive forms of Osteogenesis Imperfecta (OI) and four genes associated with bone mineral density (BMD), a key osteoporosis indicator, identified through genome-wide association studies (GWAS) were selected. The crispant screening approach, based on CRISPR/Cas9 technology, was used to phenotype directly in F0 mosaic founder zebrafish. Next-Generation Sequencing (NGS) analysis revealed a mean indel efficiency of 88% across ten different crispants, indicating a high proportion of knock-out alleles and thus resembling stable knock-out models. We applied multiple techniques to evaluate skeletal characteristics at 7, 14 and 90 days post-fertilization (dpf), including microscopy for osteoblast reporter visualization and mineralization by Alizarin Red S staining, and microCT for quantitative skeletal analysis. While larval crispants exhibited

variable differences in osteoblast-positive and mineralized surface areas, adult-stage crispants displayed more pronounced and consistent skeletal phenotypes. Notably, all crispants developed malformed neural and haemal arches, with a majority presenting vertebral fractures and fusions, and some showing significant alterations in vertebral bone volume and density. In addition, *aldh7a1* and *mbtps2* crispants experienced increased mortality due to severe skeletal deformities. RT-qPCR analysis of osteoblast differentiation and bone formation markers at larval stages indicated differential expression of osteogenic markers *bglap* and *col1a1a* in a substantial portion of the crispants, hinting at their utility as biomarkers for FBD crispant screening. In summary, our findings demonstrate that crispant screening in zebrafish offers a viable and efficient strategy for the functional assessment of FBD genes. We advocate for a novel comprehensive approach that integrates various techniques and evaluates distinct skeletal and molecular profiles across different developmental and adult stages. This methodology has the potential to provide new insights into the role of these genes in skeletal biology.

Introduction

Heritable fragile bone disorders (FBD), which are generally associated with increased fracture risk, range from common multifactorial conditions to rare monogenic diseases (Charoenngam *et al.*, 2023). They present within a wide phenotypic spectrum where monogenic disorders are generally more severe and often include skeletal deformities and extra-skeletal abnormalities. Multifactorial FBD, on the other hand, usually present with milder symptoms that are often restricted to bone fragility. Osteoporosis is a common skeletal disease characterized by low bone mass, low bone mineral density (BMD) and increased fracture risk (Kanis *et al.*, 1994). It affects about 200 million people around the world (Pouresmaeili *et al.*, 2018). In Europe, 5.6% of the population aged over 50 is diagnosed with osteoporosis, making it a highly prevalent disease, especially in the elderly. The risk of osteoporosis is influenced by both environmental factors, such as physical activity, diet preferences, medication use, coexisting diseases, and genetic factors (Ralston and Uitterlinden, 2010). Low BMD and fractures are highly heritable risk factors, with heritability values ranging from 50% to 80% (Brent Richards *et al.*, 2012). Genome-wide association studies (GWAS) in humans have unraveled hundreds of susceptible loci associated with BMD and other bone traits related to risk of osteoporotic fracture (Zhu *et al.*, 2021). GWAS results have great potential for the development of drug targets, the identification of risk factors, and risk prediction for osteoporosis. However, the identification of causal genes at these loci or the mechanisms by which GWAS loci alter bone physiology has faced challenges due to the scarcity of *in vivo* validation tools with sufficient throughput (Sabik and Farber, 2017).

In monogenic FBD, on the other hand, gene identification is generally more straightforward. One example of such a disease is osteogenesis imperfecta (OI), a genetically heterogeneous connective tissue disorder that is mainly characterized by bone fragility, skeletal deformities, and other extra skeletal manifestations (Forlino and Marini, 2016). Although in the majority of cases, it is caused by autosomal dominant mutations in the collagen type 1 genes, mutations in an increasing number of non-collagen genes causing severe recessive forms of OI, are being identified. These genes encode proteins that are involved in different aspects of bone formation, such as osteoblast differentiation (OSTERIX, WNT1, OASIS, S2P and SPARC), bone mineralization (PEDF and BRIL) and collagen processing (HSP47, FKBP65, LH2, KDELR2, CRTAP, P3H1, CyPB and TRIC-B) (Forlino and Marini, 2016)(Jovanovic *et al.*, 2022). Recent sequencing technologies have improved genetic diagnosis, but the investigation of the pathogenesis of the different forms of OI is still a laborious, costly, and time-consuming task. Hence, it is essential to develop efficient and cost-effective methods for *in vivo* functional testing to validate the involvement and mechanistic role of candidate and newly identified causal genes in the pathogenesis of FBD.

Zebrafish are a valuable model organism for studying human diseases, as they share a high degree of genetic similarity with humans. More than 70% of human protein-coding genes and 82% of human disease-related genes have zebrafish orthologs, including most of the genes involved in skeletogenesis (Howe *et al.*, 2013 [↗](#)). Additionally, zebrafish share many of their skeletal features and ossification mechanisms with mammals (Dietrich *et al.*, 2021 [↗](#)) and numerous zebrafish models for skeletal diseases have been established and investigated (Gistelink *et al.*, 2018 [↗](#)) (Daponte *et al.*, 2023 [↗](#)) (Kague and Karasik, 2022 [↗](#)). These models have some advantages over rodent models, such as longer survival, likely due to the reduced impact of gravity on their fragile skeletons in the aquatic environment, and the availability of transgenic lines marking specific bone cell types combined with the transparency of early life stages allowing for *in vivo* observation of the dynamics of skeletal development (Dietrich *et al.*, 2021 [↗](#)).

Genome-editing with CRISPR/Cas9 is a fast and easy method to create knockout alleles and stable zebrafish mutant lines (Uribe-Salazar *et al.*, 2022 [↗](#)). However, obtaining zebrafish lines that are homozygous for the mutant alleles requires two generations of adult animals (>6 months), which limits the efficiency and affordability of genetic screens (Kroll *et al.*, 2021 [↗](#)). To overcome these drawbacks, phenotyping the first-generation (F0) mosaic founder zebrafish, also known as crispants, is an emerging approach. Adult crispants have a shorter generation time (~3 months) than stable lines (6 to 9 months), which allows screening more genes in less time and at lower costs and resources. We previously demonstrated the feasibility of this approach by comparing the phenotypes and molecular profiles of a stable knockout line and a crispant for the osteoporosis gene *lrp5*, and found them to be highly similar (Bek *et al.*, 2021 [↗](#)). In a study by Watson *et al.*, 2020 [↗](#), comparison of crispants to homozygous germline mutants for *bmp1a* and *plod2*, two causal OI genes, revealed phenotypic convergence, suggesting that crispants faithfully recapitulate the biology of germline skeletal disease models. Therefore, while zebrafish crispant screens are promising as an economic, fast, and biologically relevant genetic screening approach in vertebrate model systems, a rigorous evaluation of their potential to screen for FBD-associated genes is needed.

In this study, we aimed to conduct a pilot-study to evaluate the feasibility of zebrafish crispant screening as a gene-based approach for rapid *in vivo* functional screening and validation of a set of causal genes for a broad range of FBD. The selected set includes on one hand genes associated with traits related to osteoporosis which is a relatively mild late-onset FBD and on the other hand genes causing recessive forms of OI associated with more severe skeletal phenotypes. An overview of the selected genes with observed mutant phenotypes in human, mice and zebrafish is provided in Supplementary Table 1. With this study, we want to provide an experimental platform for medium-sized zebrafish crispant screening of FBD genes.

Results

Generation of zebrafish crispants for osteoporosis and OI genes

To identify and prioritize potential causal genes for osteoporosis, we used the GWAS catalog (Sollis *et al.*, 2023 [↗](#)). We selected the variants associated with bone density and ranked them by their GWAS evidence, i.e., the number of independent publications that reported significant associations. We then identified the genes that harbored these variants and chose the top four candidates with single zebrafish orthologs: *ALDH7A1*, *ESR1*, *DAAM2* and *SOST*. Furthermore, we selected six genes associated with recessive forms of OI associated with severe skeletal phenotypes, and involved in different aspects of bone formation, including osteoblast differentiation (*CREB3L1*, *MBTPS2* and *SPARC*), bone mineralization (*SERPINF1* and *IFITM*) and collagen transport (*SEC24D*).

For each of the 10 selected genes and “scrambled” sequence, Alt-R™ gRNAs (IDT) were designed through a thorough procedure, via the Benchling platform. For each gene, the gRNA with the highest out-of-frame (OOF) efficiency, as predicted by the InDelphi-mESC prediction tool (Supplementary Figure 1), was selected for co-injection with Cas9 into one-cell stage embryos. Based on previous studies, we assumed that high indel (insertion/deletion) and OOF efficiencies result in a sufficient reduction or inactivation of the corresponding protein in crispants to induce a skeletal phenotype (Naert *et al.*, 2020 [↗](#)). DNA from a pool of 1 dpf larvae (n=10) for the different crispants and corresponding sibling controls, was extracted, and subjected to NGS analysis. Sequencing data was analyzed using the Crispresso2 tool (Clement *et al.*, 2019 [↗](#)) to determine the fraction of reads containing indels, the OOF rate and the number of in-frame deletions consisting of more than 6 base pairs in these pools (Table 1 [↗](#)).

Across the different crispants the minimal indel efficiency was 71%, while the OOF rate ranged between 49 and 73%. We subsequently determined the proportion of reads containing in-frame deletions of at least 6 base pairs, resulting in the removal of 2 or more amino acids (Table 1 [↗](#); Supplementary Figure 1). Such deletions have a relatively high chance of impairing protein function (Emond *et al.*, 2020 [↗](#))(Savino *et al.*, 2022 [↗](#))(Miton and Tokuriki, 2023 [↗](#)). The accumulated percentage of reads with indels that likely cause loss-of-function of the respective protein (OOF % + % in-frame indel $\geq$ 6bp), fall within the range of 60% to 92%, although also reads with short in-frame indels (<6bp) can affect protein function. Finally, we investigated the occurrence of off-target effects in these samples by analyzing NGS data from the three most probable off-target sites per crispant, as determined by the CFD score provided by the CRISPOR tool (Concordet and Haeussler, 2018 [↗](#)). In 20 out of the 30 examined off-target sites, no off-target mutations were identified (Supplementary Table 2). For the remaining off-target sites, the off-target rate ranged from 0,11% to 2,82%. This included basepair substitutions which are most likely sequencing errors, or true off-target indel variants, present in such low number of genomes that it is negligible in terms of biological impact in the crispants.

Assessment of the early skeleton in crispants reveals differences in osteoblast-positive and mineralized surface areas

Crispant and sibling controls were raised until 7 or 14 dpf. At this point the presence of immature osteoblasts in the head region was visualized using the transgenic *osx:Kaede* background. Images from 10 larvae per crispant were captured from the ventral perspective at 7dpf and from both ventral and lateral perspectives at 14dpf, as this provides a more comprehensive view of the opercle's surface area that can be clearly visualized at that time. The osteoblast-positive areas in both the total head and the opercle were then quantified to gain insight into the formation of new skeletal tissue during early development (Figure 1a [↗](#); Supplementary Figure 2, 3).

At 7 and 14 dpf, *esr1* crispants exhibited a significant increase of the osteoblasts-positive surface area within the head ($p \leq 0,05$; $p \leq 0.001$) (Figure 1b [↗](#), 1c [↗](#)). Additionally, *ifitm5* crispants at 14 dpf also displayed a significant increase ($p \leq 0.01$) in osteoblasts-positive surface area within the head. Finally, the increased osteoblasts-positive surface area was also observed in the opercle of both crispants at 14 dpf (*esr1* $p \leq 0.001$; *ifitm5* $p \leq 0.01$) and in the opercle of *serpinf1* ($p \leq 0.01$) and *sparc* ($p \leq 0.05$) crispants.

Subsequently, Alizarin Red S (ARS) staining was conducted on the same 7 and 14 dpf crispant zebrafish larvae in order to evaluate the degree of mineralization in the early skeletal structures. Ventral views were captured at 7 dpf, while both ventral and lateral views were obtained at 14 dpf. These lateral images at 14 dpf served a dual purpose: they facilitated measurement of the mineralized surface area of the opercle and allowed for quantification of the number of mineralized vertebrae. We quantified the mineralized surface areas of the total head, the notochord tip, and the opercle, as well as determined the number of vertebrae (Figure 1a [↗](#); Supplementary Figure 4, 5).

	<i>aldh7a1</i>	<i>daam2</i>	<i>esr1</i>	<i>sost</i>	<i>creb3l1</i>	<i>ifitm5</i>	<i>mbtps2</i>	<i>sec24d</i>	<i>serpinf1</i>	<i>sparc</i>
% reads with indel	87%	96%	92%	80%	71%	90%	94%	85%	92%	92%
% reads with out-of-frame indel	66%	57%	64%	64%	49%	73%	73%	63%	55%	72%
% reads with in frame indel $\geq$ 6-bp	16%	24%	15%	14%	11%	15%	19%	12%	25%	16%
% reads likely affecting protein function	82%	81%	79%	78%	60%	88%	92%	75%	80%	88%

Table 1

InDelphi-mESC prediction, indel, out-of-frame indel and in-frame rates for the different crispants, determined by NGS from pools of 1dpf embryos. The first four genes are associated with the pathogenesis of osteoporosis, while the last six are linked to osteogenesis imperfecta. The percentage of reads likely to affect the protein function is calculated based on the percentage of reads with out-of-frame indels combined with the percentage of reads with in-frame deletions of equal to or more than 6 basepairs.

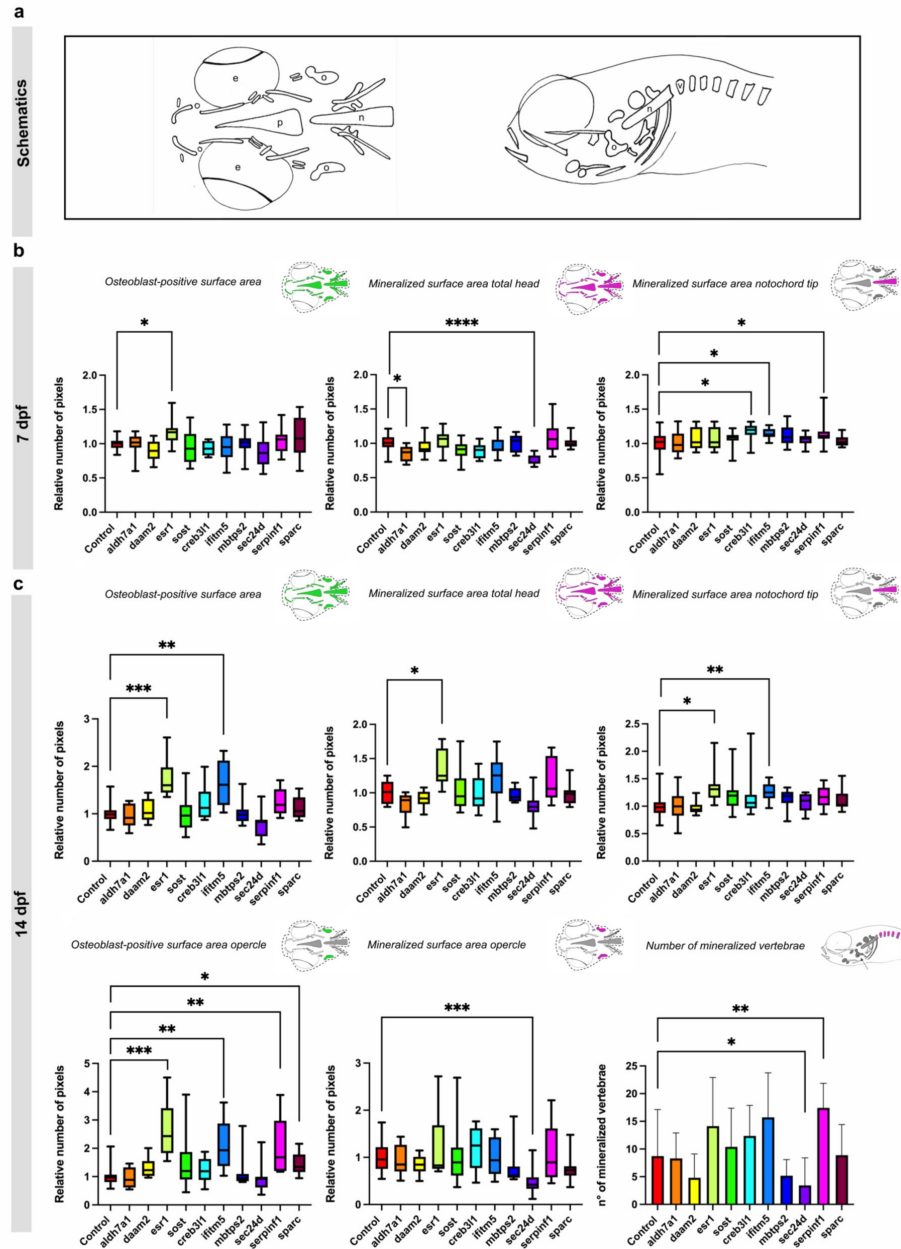


Figure 1

Measurements of osteoblast-positive surface area and mineralized surface area of the head skeleton in 7 and 14 dpf crispants. The first four genes are associated with the pathogenesis of osteoporosis, while the last six are linked to osteogenesis imperfecta. (a) Schematic overview of the ventral and lateral perspective of the head of zebrafish larvae at 7 and 14 dpf. The surface area of the total head is circled with a dashed line. Arrows point to the notochord tip (n), the opercle (o) and the mineralized vertebrae. The eyes (e) and parasphenoid (p) are also shown. (b) Quantification of the osteoblast-positive surface area of the total head and the mineralized surface area of the total head and notochord tip at 7 dpf in comparison with their respective controls. (c) Quantification of the osteoblast-positive surface area of the total head and the mineralized surface area of the total head, opercle and notochord tip and number of vertebrae at 14 dpf in comparison with their respective controls. For easier visualization, obtained results were normalized to the respective controls (normalization = individual value crispant (or control) / mean control) (n=10). Statistical significance is evaluated using the Mann-Whitney U - test on non-normalized data and significant differences were visualized using an asterisk (* = $p \leq 0,05$; ** = $p \leq 0,01$; *** = $p \leq 0,001$; **** = $p \leq 0,0001$). Error bars show the standard deviation of non-normalized data.

At 7dpf, the total head exhibited a significant reduction in mineralized surface in *aldh7a1* ($p \leq 0.05$) and *sec24d* crispants ($p \leq 0.0001$), while the notochord tip displayed a significant increase in mineralized surface area in *creb3l1* ($p \leq 0.05$), *ifitm5* ($p \leq 0.05$), and *serpinf1* ($p \leq 0.05$) crispants (**Figure 1b** [↗](#)). At 14 dpf, a similar trend of reduced mineralized surface area of the total head was observed in *aldh7a1* and *sec24d* crispants, albeit not reaching statistical significance. In contrast, the mineral surface area of the head was significantly increased in *esr1* crispants ($p \leq 0.05$). Furthermore, the increased mineralization of the notochord tip remained significant in *ifitm5* crispants ($p \leq 0.01$), while it normalized in *creb3l1* and *sec24d* crispants. A novel increase emerged in *esr1* crispants ($p \leq 0.05$). Finally, at 14 dpf, *sec24d* crispants exhibited a significant decrease ($p \leq 0.001$) in the mineralized surface area of the opercle and the number of mineralized vertebrae, whereas *serpinf1* crispants showed a notable increase in the number of mineralized vertebrae ($p \leq 0.01$) (**Figure 1c** [↗](#)).

RT-qPCR expression analysis reveals differential expression of osteogenic markers *bglap* and *col1a1a* in a significant subset of crispants

To explore the expression level of different osteogenic markers throughout the set of crispants, RT-qPCR analysis was performed on whole larvae at 7 and 14 dpf. At 7dpf, no significant differences were seen in the expression of *runx2*, an early pre-osteoblast marker, between the different crispants and corresponding controls. *Osterix*, also known as *sp7*, a *runx2* downstream gene which plays a critical role for the differentiation of pre-osteoblasts into mature osteoblasts, was only upregulated in crispants for *sparc* ($p \leq 0.001$). Osteocalcin, also known as *bglap*, which is mainly expressed in mature osteoblasts, was downregulated in almost all crispants, except in crispants for *sost* and *sparc*. Finally, *col1a1a*, encoding the $\alpha 1$ chain of type 1 collagen, and marking extracellular matrix synthesis by both pre- and mature osteoblasts (Valenti *et al.*, 2020 [↗](#)), was upregulated in crispants for *aldh7a1* ($p \leq 0.001$), *daam2* ($p \leq 0.05$), *esr1* ($p \leq 0.05$) and *sec24d* ($p \leq 0.05$) (**Figure 2a** [↗](#)).

At 14dpf, the expression of *runx2* remained unchanged in all crispants compared to control. The expression of *sp7* was significantly increased in crispants for *daam2* ($p \leq 0.05$) and *sec24d* ($p \leq 0.05$), decreased in *esr1* crispants, while expression levels were normalized in *sparc* crispants relative to 7 dpf ($p \leq 0.05$). The expression of *bglap* remained significantly downregulated in crispants for *aldh7a1* ($p \leq 0.001$), *daam2* ($p \leq 0.01$), *esr1* ($p \leq 0.01$) and *creb3l1* ($p \leq 0.05$) while it reverted to control levels in *ifitm5*, *sec24d* and *serpinf1* crispants. An upregulation in the expression of *col1a1a* was seen in all the crispants, except in crispants for *sparc* and for *aldh7a1* and *esr1* where expression levels normalized compared to 7dpf (**Figure 2b** [↗](#)).

Assessment of the adult skeleton in FBD crispants reveals frequent morphological abnormalities and quantitative differences in vertebral bone parameters

Crispant were further grown into adulthood (90dpf) and subjected to whole-mount ARS staining for mineralized bone, in order to identify skeletal abnormalities. Crispants for both *aldh7a1* and *mbtps2* displayed early lethality. Survival analysis indicated that *aldh7a1* crispants experienced increased lethality from 7dpf onwards, with no survivors beyond 20dpf, while *mbtps2* crispants exhibited increased lethality from 17dpf onwards, with only a very small number of fish surviving into adulthood (90dpf) (**Figure 3** [↗](#)). ARS staining of the skeleton of two surviving adult *mbtps2* crispant fish revealed severe cranial malformations, including underdevelopment of the premaxilla, dentary, and articular. However, the vertebral column seemed to be only mildly affected.

Figure 2

RT-qPCR expression analysis of *runx2*, *sp7*, *bglap* and *col1a1a* in crispants at 7 (a) and 14 dpf (b) and their respective controls, normalized according to the controls (normalization = individual values crispant (or control) / mean control). The first four genes are associated with the pathogenesis of osteoporosis, while the last six are linked to osteogenesis imperfecta. Statistical significance is evaluated using the Mann-Whitney U test on non-normalized data and significant differences were visualized using an asterisk (* = $p \leq 0,05$; ** = $p \leq 0,01$; *** = $p \leq 0,001$; **** = $p \leq 0,0001$). Error bars show the standard deviation of non-normalized data.

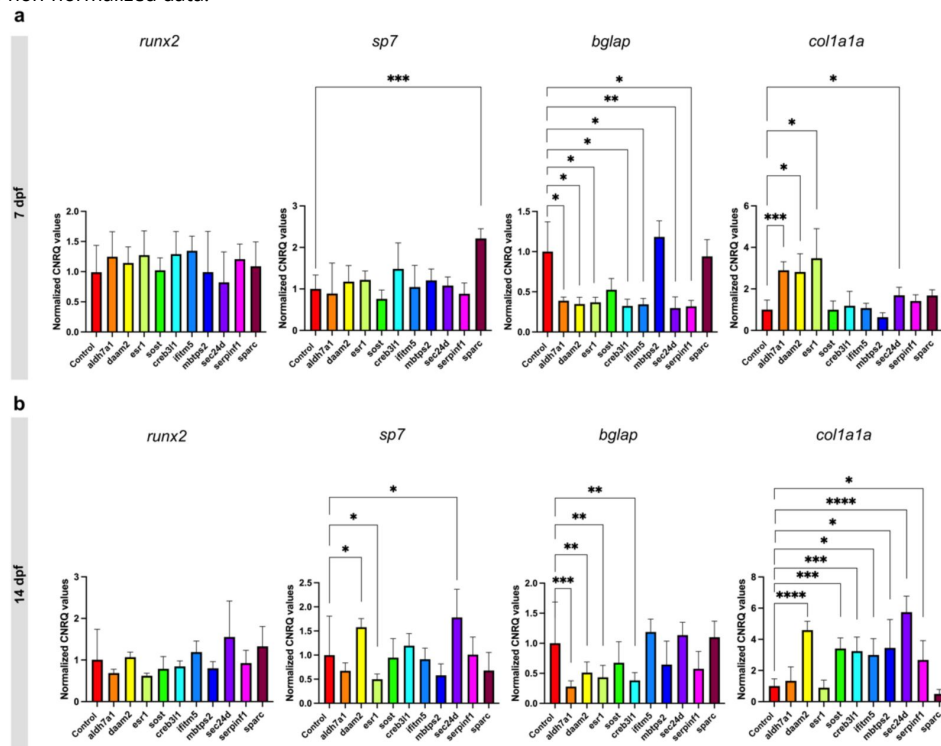
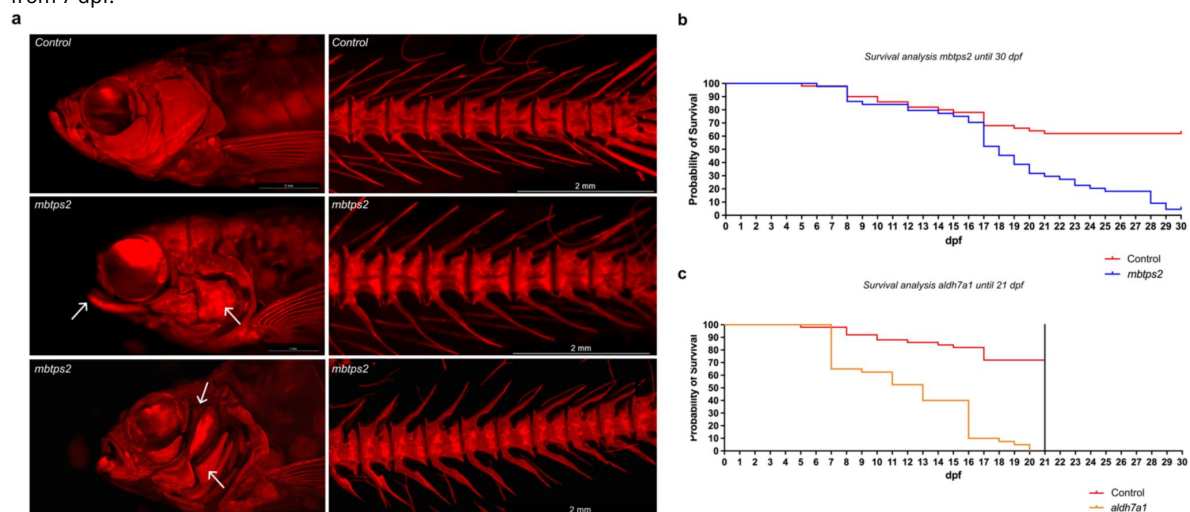


Figure 3

ARS images and survival analysis of *mbtps2* crispants. (a) ARS images of control fish and crispants for *mbtps2*, showing severe craniofacial abnormalities (arrows). (b) Survival curve of controls and crispants for *mbtps2*, showing a reduction in survival starting from 17 dpf. (c) Survival curve of controls and crispants for *aldh7a1*, showing a reduction in survival starting from 7 dpf.



Among the eight crispants that successfully matured into adulthood, none exhibited significant differences in standard length and head size ($n=5$ fish per crispant) (**Figure 4b**). However, *esr1* crispants were observed to have notably larger eye diameters (**Figure 4b**). All these crispants demonstrated various abnormalities in the caudal part of the vertebral column such as fusions, compressions, fractures, or arch malformations, except for *daam2* crispants where no obvious abnormalities were detected (**Figure 4a,c**; Supplementary Figure 6). In *creb3l1* crispants the vertebral phenotype was relatively mild and primarily restricted to arch malformations.

Next, the adult skeleton of the different crispants and sibling controls was visualized by microCT scanning and the data was quantified and further analyzed using FishCuT software (Hur *et al.*, 2017). For each of the vertebral centra, the length, tissue mineral density (TMD), volume, and thickness were determined and tested for statistical differences between groups using a regression-based statistical test (Supplementary Figure 7). To quantify the extent of differences between crispants and their controls, the means of these parameters in the crispants' vertebral column, were normalized to the standard deviation of the controls, resulting in a z-score [$\text{z-score} = (\text{mean crispant} - \text{mean control}) / \text{SD control}$] (Gistelink *et al.*, 2018). A significant increase in centrum volume was observed in *daam2* crispants compared to the controls ($p < 0.05$, $z = 2.86$) (**Figure 4d**). Centrum TMD was significantly higher, and to a similar extent, in crispants for *daam2* ($p < 0.05$; $z = 1.54$), *esr1* ($p < 0.05$; $z = 1.62$), and *sost* ($p < 0.05$; $z = 1.41$), three genes likely involved in osteoporosis pathogenesis. Centrum thickness was increased in crispants for *esr1* ($p < 0.05$; $z = 4.26$), *ifitm5* ($p < 0.01$; $z = 7.13$), and *sec24d* ($p < 0.05$; $z = 5.04$) with the most pronounced increase observed in *ifitm5* crispants. Centrum length was increased only in *daam2* crispants ($p < 0.05$; $z = 4.22$).

Discussion

The generation of a diverse array of null alleles through CRISPR/Cas9-induced F0 mosaic (crispant) zebrafish offers specific advantages compared to stable knockout zebrafish lines, in particular for rapid screening of phenotypes (Naert *et al.*, 2020). In this study we tested the efficacy of a semi-high throughput zebrafish crispant analysis for rapid validation of candidate disease causing genes for skeletal disorders across a broad phenotypic spectrum. On one hand we included genes for non-classical recessive OI, which is an early-onset monogenic skeletal syndrome with severe skeletal deformities. On the other hand, we screened a set of top candidate genes for osteoporosis, which is a rather late-onset multifactorial disease with little to no deformities. All selected genes show skeletal expression in both human and zebrafish. An overview of the selected genes with observed mutant phenotypes in human, mice and zebrafish is provided in Supplementary Table 1. It is important to note that this study focused on candidate genes for osteoporosis, not on the role of specific variants identified in GWAS studies. Non-coding variants for instance, which are often identified in GWAS studies, present significant challenges in terms of functional validation and interpretation. In this study we propose a crispant screening platform that combines various phenotypic and molecular assays at three key developmental and adult stages (7, 14 and 90 dpf). To obtain a general overview of the results for the selected crispants, all results were summarized in **Table 2**.

At two distinct larval stages, 7 dpf and 14 dpf, diverse measurements of the early skeleton were conducted, including an assessment of both the osteoblast-positive and the mineralized surface areas located in the head region. The osteoblast-positive area represents the quantity of osteoblasts within a given structure and is a measure of the formation of bone matrix. Although a general tendency towards increased areas could be noted across different crispants at 14dpf, only crispants for *esr1* showed a consistent increase at both 7 and 14 dpf. Interestingly, Brett *et al.*, 2021 extensively investigated *esr1* mutations in the context of hormone receptor-positive breast

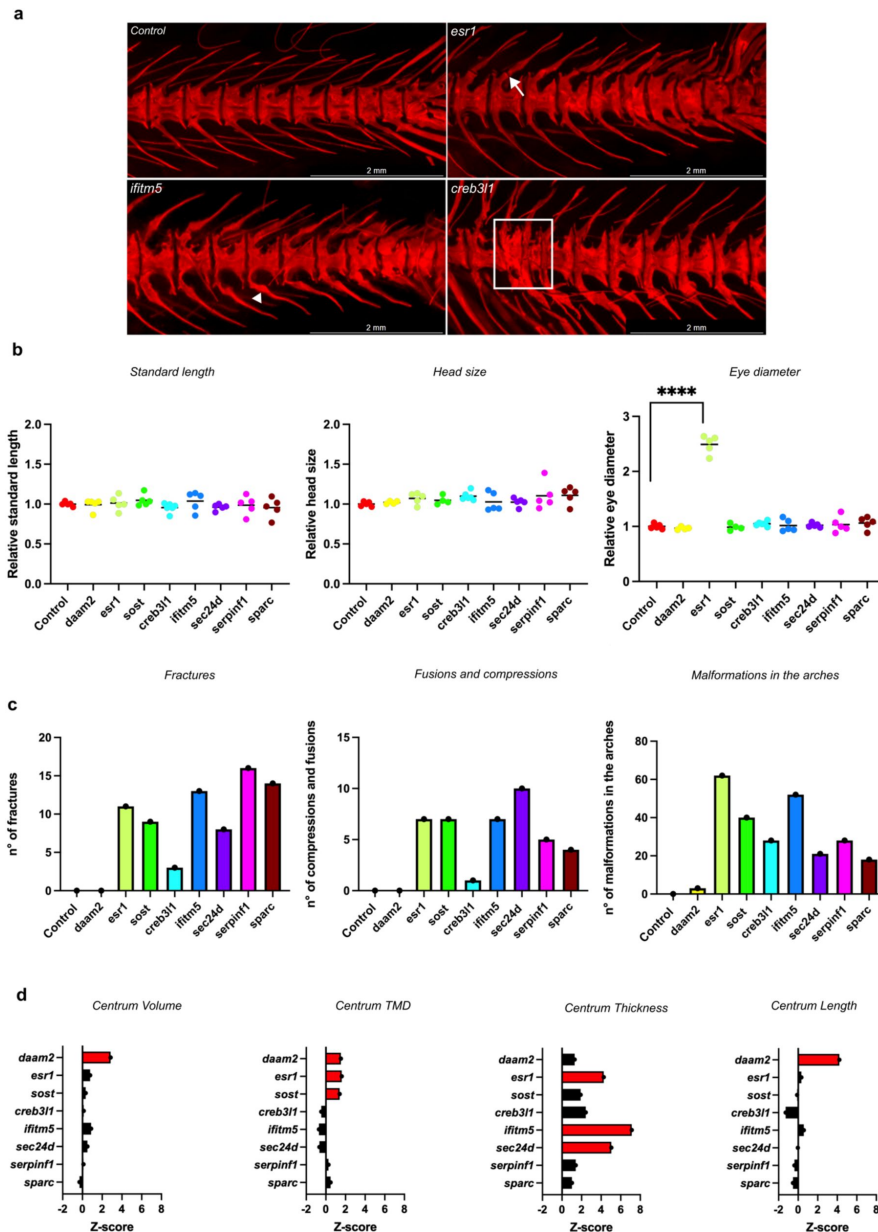


Figure 4

Skeletal phenotyping of adult crispants and their respective controls. The first three genes are associated with the pathogenesis of osteoporosis, while the last five are linked to osteogenesis imperfecta (a) Pictures of ARS-stained vertebral column of a control and three crispants (from left to right: *esr1*, *ifitm5* and *creb3l1*), showing fractures (arrow), fusions and compressions (squared) and malformations in the arches (arrowhead). (b) Measurements of the standard length, the head size and the eye diameter of the crispants compared to their control. The standard length was measured from the snout tip to the tail base. The head size was measured from the snout tip to the supraoccipital bone and the eye diameter was measured from the lateral ethmoid to the hyomandibula. The data was normalized for easier visualization (normalization = individual value crispants (or controls) / mean control) (n=5)). (c) Quantification of the number of fractures, fusions or compressions and malformations in the arches of crispants and the controls. For this quantification, twelve vertebrae were selected per fish and a total of 5 crispants per assay was evaluated. Statistical analysis was evaluated using the Mann-Whitney U -test on non-normalized data and significant differences were visualized using an asterisk (* = $p \leq 0,05$; ** = $p \leq 0,01$; *** = $p \leq 0,001$; **** = $p \leq 0,0001$). Error bars showed the standard deviation of non-normalized data. (d) Quantification of skeletal parameters by quantitative micro-computed tomography (μ CT) analysis. In the graphical representation, the different crispants were listed. Statistically significant differences from the control values for a given crispant were depicted as red bars. Significance levels were determined through the global test analysis (Supplementary Figure 7).

	<i>aldh7a1</i>	<i>daam2</i>	<i>esr1</i>	<i>sost</i>	<i>creb3l1</i>	<i>ifitm5</i>	<i>mbtps2</i>	<i>sec24d</i>	<i>serpinf1</i>	<i>sparc</i>
Osteoblast-positive surface area total head										
7 dpf	ns	ns	(+)*	ns	ns	ns	ns	ns	ns	ns
14 dpf	ns	ns	(+)**	ns	ns	(+)**	ns	ns	ns	ns
Osteoblast-positive surface area operculum 14 dpf	ns	ns	(+)**	ns	ns	(+)**	ns	ns	(+)**	(+)*
Mineralized surface area total head										
7 dpf	(-)*	ns	ns	ns	ns	ns	ns	(-)**	ns	ns
14 dpf	(-)*	ns	ns	ns	ns	ns	ns	ns	ns	ns
Mineralized surface area notochord tip										
7 dpf	ns	ns	ns	ns	(+)*	(+)*	ns	(+)*	ns	ns
14 dpf	ns	ns	(+)**	ns	ns	(+)*	ns	ns	ns	ns
Mineralized surface area operculum 14 dpf	ns	ns	ns	ns	ns	ns	ns	(-)**	ns	ns
Number of mineralized vertebrae 14 dpf	ns	ns	ns	ns	ns	ns	ns	(-)**	ns	ns
<i>runx2</i> expression										
7 dpf	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
14 dpf	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
<i>sp7</i> expression										
7 dpf	ns	ns	ns	ns	ns	ns	ns	ns	ns	(+)**
14 dpf	ns	(+)*	(-)*	ns	ns	ns	ns	(-)*	ns	ns
<i>bglap</i> expression										
7 dpf	(-)*	(-)*	(-)*	ns	(-)*	(-)*	ns	(-)*	(-)*	ns
14 dpf	(-)**	(-)**	(-)**	ns	(-)**	ns	ns	ns	ns	ns
<i>coll1a1</i> expression										
7 dpf	(+)**	(+)*	(+)*	ns	ns	ns	ns	(+)*	ns	ns
14 dpf	ns	(+)**	ns	(+)**	(+)**	(+)*	(+)**	(+)**	(+)*	ns
Standard length 90 dpf		ns	ns	ns	ns	ns		ns	ns	ns
Head size 90 dpf		ns	ns	ns	ns	ns		ns	ns	ns
Diameter eye 90 dpf		ns	ns	ns	ns	ns		ns	ns	ns
Centrum Volume 90 dpf		(+)*	ns	ns	ns	ns		ns	ns	ns
Centrum TMD 90 dpf		(+)*	(+)*	(+)*	ns	ns		ns	ns	ns
Centrum Thickness 90 dpf		ns	(+)*	ns	ns	(+)*		(+)*	ns	ns
Centrum Length 90 dpf		(+)*	ns	ns	ns	ns		ns	ns	ns

Table 2

Overview of the different measurements in crispants at 7, 14 and 90 dpf. The first four genes are associated with the pathogenesis of osteoporosis, while the last six are linked to osteogenesis imperfecta. (-): downregulation or less, (+) upregulation or more, ns: not significant, asterisk defines statistical significance (* = p σ ; 0,05; ** = p σ ; 0,01; *** = p σ ; 0,001; **** = p σ ; 0,0001).

cancer but did not evaluate the presence of osteoblasts. However, the depletion of estrogen in an osteoblastic cell line *in vitro* results in the stimulation of osteoblast differentiation (Schiavi *et al.*, 2021 [DOI](#)).

The extent of mineralization of the head skeletal elements was found to be mostly not different compared to controls, although in the crispants where significant differences were detected at one of the studied time points, the mineralization of the head skeleton elements was mostly lower and of the notochord tip higher. Only crispants for *sec24d*, a gene critical for transporting extracellular matrix (ECM) proteins, exhibited reduced mineralization in different head structures both at 7dpf and 14dpf. These findings aligned with the observed malformations in *bulldog* zebrafish, where disrupted *sec24d* function leads to head abnormalities and growth delays in early larval stages (Sarmah *et al.*, 2010 [DOI](#)). Although the measurements of osteoblast-positive and mineralized surface areas may be influenced by size differences among some of the crispants, normalization to size parameters was not conducted, as variations in growth were considered integral to the phenotypic outcome.

Despite considerable variability in the measurements we conducted, a subtle trend emerged in the expression data for osteogenic markers during early stages. Specifically, the expression of *bglap*, a late osteoblast differentiation marker appeared to be consistently downregulated in near all crispants, except for crispants for *sost*, *mbtps2* and *sparc* at 7 dpf. However, this downregulation became less pronounced at 14 dpf, affecting only crispants for *aldh7a1*, *daam2*, *esr1* and *creb3l1*. Interestingly, most crispants for genes involved in the pathogenesis of osteoporosis exhibited this downregulation, except for *sost*, where the expression of *bglap* remained unaffected. In contrast, the expression of *col1a1a* showed an opposing trend. Initially, a modest upregulation of this marker was observed at 7 dpf, limited to just four crispants. However, this effect intensified over time, with nearly all crispants displaying upregulation at 14 dpf, except for *aldh7a1*, *esr1*, and *sparc*. The remarkable upregulation of *col1a1* expression could potentially arise from an abundance of immature osteoblasts within the cranial skeleton, a phenomenon we frequently observed across the set of crispants (Amarasekara *et al.*, 2021 [DOI](#)). These osteoblasts play an active role in the synthesis of the organic bone matrix, including the production of collagen type I fibers. Interestingly, the generally diminished expression of the late osteoblastic marker *bglap* corroborates the presence of less mature osteoblasts (Gavaia *et al.*, 2006 [DOI](#)). As mainly mature osteoblasts engage in the deposition of calcium and phosphate ions, essential for the formation of hydroxyapatite crystals, bone mineralization can be expected to be reduced in the crispants, which results in increased formation of non-mineralized osteoid deposits. Indeed, we observed that despite often increased bone osteoblast-positive surfaces, mineralization-positive areas in the head skeleton were frequently found to be reduced (Salhotra *et al.*, 2020 [DOI](#)). The differential expression profiles of the osteogenic markers *bglap* and *col1a1a* highlight their potential as biomarkers for osteoblast differentiation and bone formation in FBD crispant screens. However, it is important to note that the genes evaluated by RT-PCR are not exclusively expressed in bone tissue. Since whole-body samples were used for expression analysis, there is a possibility that the observed changes in gene expression may be influenced by other non-skeletal cell types.

In early stages of development, we observed that crispants, although presenting with a high indel frequency, showed a relatively high variability for the phenotypic parameters we tested (mineralization and osteoblast surface areas), which often prevented reaching statistical significance. Phenotypic variability in these zebrafish larvae can be attributed to several factors, including crispant mosaicism, allele heterogeneity, environmental factors, differences in genomic background and development, maternally-deposited RNAs, and slightly variable imaging positioning. In our study, for each crispant and corresponding controls, all experiments at different ages were conducted on zebrafish from the same clutch, allowing analysis of a developmental time series in animals with a relative genetically homogeneous background. Although increasing the number of biological replicates could potentially enhance statistical power, previous studies have not confirmed this (Winter *et al.*, 2022). Enhancing out-of frame

(OOF) rates by simultaneously targeting a single gene with multiple crRNAs could potentially increase the penetrance of phenotypic abnormalities observed in early crispants. By directing crRNAs to multiple loci within one gene, the likelihood of introducing frameshift mutations increases significantly. This is suggested to lead to a higher rate of biallelic knockout and reduce the chances of retaining the functional protein (Kroll *et al.*, 2021 [↗](#)). However, this also elevates the likelihood of off-target effects, increases double-strand breaks and toxicity, while simultaneously increasing costs (Wu *et al.*, 2018 [↗](#)). Furthermore, also in-frame indels affecting two or more amino acids, detected in a substantial proportion of NGS reads in our study, are likely to have a detrimental effect on protein function (Emond *et al.*, 2020 [↗](#))(Savino *et al.*, 2022 [↗](#))(Mito and Tokuriki, 2023 [↗](#)). Therefore, and because we used highly efficient two-part guide RNAs (Alt-R™ CRISPR-Cas9 system, we opted for single crRNA injections. While there remains a possibility of false negatives, the overall indel efficiency, as indicated by our NGS analysis, is high (>90%), thereby reducing the likelihood of having crispants with very low indel efficiency.

In adult crispants, the skeletal phenotype was generally more penetrant. All crispants showed malformed arches, a majority displayed vertebral fractures and fusions and some crispants exhibited distinct quantitative variations in vertebral body measurements. Additionally, these skeletal malformations were consistently observed in a second clutch of crispants (Supplementary Figure 8), underscoring the reproducibility of these phenotypic features across independent clutches. This confirmed the role of the selected genes in skeletal development and homeostasis and their involvement in skeletal disease and established the crispant approach as a valid approach for rapidly providing *in vivo* gene function data to support candidate gene identification.

Osteoporosis is typically linked with symptoms that appear late in life. However, our results challenged this notion, by showing that in crispants for osteoporosis genes, skeletal abnormalities can manifest earlier and are not solely reflected in changes to bone mineral density (BMD). For instance, we found that *aldh7a1* and *esr1* crispants displayed significant skeletal anomalies already at larval stages, with *aldh7a1* crispants showing early lethality. At adult stages, *esr1* and *sost* crispants demonstrated various morphological abnormalities of the vertebral column such as fusions, compressions, and arch malformations. The more pronounced and earlier phenotypes in these zebrafish crispants are most likely attributed to the quasi knock-out state of the studied genes, while more common less impactful variants in the same genes result in typical late-onset osteoporosis (Laine *et al.*, 2013 [↗](#)). This phenomenon is also observed in knock-out mouse models for these genes (Melville *et al.*, 2014 [↗](#))(Coughlin *et al.*, 2019 [↗](#)).

Interestingly, all adult crispants for osteoporosis genes demonstrated a substantial increase in centrum Tissue Mineral Density (TMD). TMD is quantitative measure of the actual mineral volume within bone tissue, computed as bone mineral content over the bone volume (mgHA/cm³) and obtained through mCT or pQCT. In human patients, reduced bone mineral density (aBMD), a measure for the bone mineral content in a projected bone area and assessed using dual energy X-ray absorptiometry (DXA), is frequently linked to osteoporosis. However, also TMD, or vBMD, can be evaluated in the trabecular and cortical bone. Knock-out mice lacking *Sost* showed an increase in TMD within the cortical bone, which is comparable to the bone present in the zebrafish vertebral column (Li *et al.*, 2008 [↗](#)). As for the other genes, for *daam2*, mutant mice with a hypomorphic *Daam2* allele presented with reduced bone strength and increased cortical bone porosity (Morris *et al.*, 2019 [↗](#)). *ERa* knockout mice presented with a decrease in cortical bone mineral density and increase in trabecular bone mineral density (Melville *et al.*, 2014 [↗](#)). Further studies are needed to better understand how high TMD values observed in these crispants relate to phenotypic changes observed in these mouse models. Finally, it is worthwhile to note that, osteoporosis typically correlates with low vBMD values. While neither the causal variant nor the biological direction of its effects on the target gene are known for BMD-associated loci harboring these genes, the increased TMD following gene knockdown in our models may help to assign the

directionality of their effects, and puts forth the possibility that variants at these loci alter the expression of genes that converge on a common biological process that in zebrafish, when disrupted results in the high TMD.

Conversely, crispants for genes involved in recessive forms of OI, an early-onset severe skeletal disorder, can intuitively be expected to exhibit pronounced skeletal abnormalities already in larval stages. Interestingly, during these early stages, the majority of the crispants do not exhibit consistent skeletal abnormalities. Although this could be partially explained by the above-discussed variability of the phenotypic outcomes we measured, also human OI subjects with these severe conditions, often experience disease onset during infancy only, with progressive worsening of the skeletal phenotype (Selina *et al.*, 2023 [DOI](#)).

The phenomenon of genetic compensation could play a role in explaining why early phenotypes manifest differently in human patients compared to zebrafish. Genetic compensation ensures an organism to maintain its genetic robustness, even when genetic variation, possibly induced by mutations, occurs. This compensation mechanism can be triggered by the upregulation of compensating genes, often mediated through the regulation of nonsense-mediated decay (NMD) in combination with the epigenetic machinery in zebrafish (El-Brolosy Mohamed A. and Stainier, 2017 [DOI](#)) (Jakutis and Stainier, 2021). Crispants, in contrast to morphants, also undergo NMD although in a mosaic manner. In larval crispant, compensatory mechanisms may effectively mask the impact of gene loss. However, in adult crispants, the cumulative effect of this loss becomes more pronounced, leading to a later onset phenotype. Furthermore, specific tissues or cell types within the organism may activate compensatory pathways more efficiently, thereby influencing the overall manifestation of the phenotype. When a gene is disrupted in humans, the consequences can be more severe due to the complexity of human development and biology. Such disruptions may result in developmental abnormalities, leading to an early onset of phenotypic traits (Rouf *et al.*, 2023 [DOI](#)). To conclude, our study proposes a multifaceted gene-based approach to investigate zebrafish crispants associated with heritable FBDs, employing various techniques, and assessing different skeletal phenotypes and molecular profiles at distinct developmental stages. While this work represents a pioneering effort in establishing a screening platform for skeletal diseases, it offers opportunities for future improvement and refinement. For instance, analyzing different skeletal structures and cell types within various transgenic lines, increasing sample size, and incorporating a broader range of techniques, such as phenotypic scoring based on the type of malformations seen in the vertebral column or alcian blue staining for cartilage tissue evaluation, could enhance the comprehensiveness of the screening process and the skeletal phenotype. Moreover, to explore the underlying mechanisms contributing to disease phenotypes, it is essential to establish stable knockout mutants derived from the crispants. Nonetheless, our initial set-up demonstrates the feasibility of this approach to identify genes potentially implicated in the pathogenesis of skeletal disorders, as all studied crispants exhibit skeletal abnormalities in adult stages. These findings support the prospect of crispant screening as a promising tool for rapid functional assessment of candidate genes for skeletal disorders, providing valuable insights into the roles of these genes in skeletal biology.

Materials and methods

Zebrafish maintenance and breeding

The zebrafish were incubated at 28°C until 5 days post-fertilization (dpf). Then, they were reared in a rotifer/zebrafish polyculture system from 5dpf to 9dpf following the method of Lawrence *et al.*, 2016 [DOI](#). After 10dpf, they were transferred to 3.5 liter tanks in the Core Zebrafish Facility Ghent (ZFG) and housed in semi-closed recirculating systems (Tecniplast). The water parameters were maintained at 27°C, pH 7.5, conductivity 550 µS, and a 14/10 light/dark cycle. The zebrafish were fed with Zebrafeed (Sparos) and Gemma Micro dry food (Inve) in the morning and Micro Artemia

(Ocean Nutrition) in the afternoon. The *osx:Kaede* transgenic line was used for all experiments. Breeding and embryo collection were done according to standard protocols (Westerfield, 2000). All animal studies complied with EU Directive 2010/63/EU for animals, permit no. ECD 23/27 (Ghent University). Pain, distress, and discomfort were minimized as much as possible.

Generation of crispants through CRISPR/Cas9 genome editing

Guide RNA design

For the generation of crispants we largely followed the methods described in Bek et al. (2021). In summary, two-part guide RNAs (gRNAs) were used which are functional gRNA duplexes made of a universal 67 mer trans-activating CRISPR-RNA (tracrRNA) and a target-specific CRISPR-RNA (crRNA) (Alt-R™ CRISPR-Cas9 System, IDT). A non-specific crRNA (GCAGGCAAAGAATCCCTGCC), referred to as the ‘scrambled’ sequence, was used to generate the controls (Wu et al., 2018).

The crRNAs corresponding to the genes of interest were designed with the web-based tool Benchling (<https://benchling.com>), using GRCz11 as a reference genome. With this tool, 20 bp crRNAs target sequences, that are followed by a ‘NGG’ PAM sequence, were listed. Further selection was based on a few specific criteria to minimize the risk of producing (partially) active truncated protein products and potential off-target effects. Specifically, crRNA target sequences located in exon 1, in the last exon, within the last 55bp of the second-to-last exon or in exons consisting of (n) x 3 bp were excluded. Additionally, crRNAs with the highest possible scores for both on-target (Doench et al., 2016) and off-target (Hsu et al., 2013) were selected.

For the selected crRNA sequences, the Indelphi tool (<https://indelphi.giffordlab.mit.edu>) employing the mESC training set, was used to predict the DNA repair outcomes (mixture of indels) resulting from non-homologous end-joining (NHEJ) and microhomology-mediated end-joining (MMEJ) induced by CRISPR/Cas9 cleavage. The crRNAs that were predicted to result in high percentages of out-of-frame indels and a limited number of possible genotypes (high precision) were prioritized.

Eventually, 1 crRNA per gene was ordered from IDT (<https://www.idtdna.com>): *aldh7a1* (AATTGTTTCGACAGATTGGAG), *daam2* (GATCTATTGCAGTAAGAAGA), *esr1* (GCTCAGACAGAAACACAGC), *sost* (CTGCTCACTCCCGCACCCAG), *creb3l1* (ACACAGTTACTCTCTCAGCG), *ifitm5* (AGCGCAGGAATGCTCAGACA), *mbtps2* (TTCCATATCAAGTGGCACAC), *sec24d* (GCCTATGGATCTCCAACACA), *serpinf1* (CAGGTTGTAGCCAAAATCAG), *sparc* (AGAGGAGCCAGCTGTTGAAG).

To predict the potential off-target effects of the selected crRNAs, Crispor (<http://crispor.tefor.net>) was used. The cutting frequently determination (CFD) off-target score was used to predict the probability of off-target cleavage. The three targets with the highest CFD scores were selected and PCR-amplified (Supplementary Table 2). Next-generation sequencing using the Miseq platform was used to assess the frequency of the off-target effects (Concordet and Haeussler, 2018).

Injection

To prepare gRNA duplexes for each assay, we mixed 200μM crRNA and 200μM tracrRNA, heated the mixture at 95°C for 5 minutes, and then cooled it to room temperature. Next, we micro-injected one-cell-stage *Tg(osx:Kaede)* zebrafish embryos. The injection mix consisted of a 1.4 nL drop containing RNase-free water, KCl (2000 mM) and ribonucleoproteins (RNPs), consisting of 800 pg of both gRNA duplex and Cas9 (1000 ng/μl) (ToolGen, Seoul, South Korea; wild-type nuclease with nuclear localization signal) protein. For each crispant and each corresponding control, a total of 200 eggs, originating from the same clutch, were injected.

Next-generation sequencing analysis

We extracted DNA from 10 pooled embryos at one day after fertilization by adding 100 µl NaOH and incubating the samples at 95°C for 20 minutes. We then added 10µL Tris-HCl. We performed PCR amplification with the primers listed in Supplementary Table 3, using either ‘FORD58’ or ‘FORD60’ assays depending on the primer. The thermocycling conditions for the ‘FORD58’ assay were: 95°C for 3 min, followed by 40 cycles of 95°C for 15s, 58°C for 10s, and 72°C for 15s, and a final extension at 72°C for 10 min. The thermocycling conditions for the ‘FORD60’ assay were: 95°C for 3 min, followed by 40 cycles of 95°C for 15s, 60°C for 10s, and 72°C for 15s, and a final extension at 72°C for 10 min. We prepared the PCR amplicons for sequencing using the Nextera XT DNA Library Preparation Kit (Illumina, San Diego, CA, USA) and sequenced them on a MiSeq instrument (Illumina) using 2 X 250 bp cycles (Bek *et al.*, 2021 [↗](#)). We analyzed the NGS data with CRISPResso2 and determined the mean fraction of reads containing in-frame and out-of-frame indels over different samples, by exporting the allele frequency table, counting the number of reads with both in- and out-of-frame indels or out-of-frame indels only and dividing these numbers by the total number of mapped reads (Fiume *et al.*, 2019 [↗](#)). For both the indel and out-of-frame efficiency, the reads with sequencing errors and natural variants were excluded.

RNA extraction and RT-qPCR

The RNA extraction and qPCR protocol described by Bek *et al.*, 2021 [↗](#) was followed, with minor modifications; for each crisprant, RNA was extracted from 4 or 5 pools of 10 embryos at 7 dpf and 14 dpf using Trizol (Life Technologies Europe) and purified using the RNeasy Mini Kit (Qiagen) with on-column DNase I treatment (Qiagen). RNA concentrations were measured with the Little Lunatic (Unchained Labs) and cDNA was synthesized using the iScript cDNA synthesis kit (Bio-rad). Primers for skeletal marker genes were designed using NCBI Primer-BLAST (Supplementary Table 4) and primers for the housekeeping genes (*elfa* and *bactin2*) were obtained from literature (McCurley & Callard, 2008 [↗](#)).

The qPCR reaction mixture was prepared with 2.5 µL of SsoAdvanced Universal SYBR Green Supermix (Bio-rad), 5 ng of cDNA, and 250 nM of each primer. The qPCR reaction was run on a LightCycler 480 instrument (Roche) in a white 384-well plate with the following thermocycling conditions: initial denaturation step at 95 °C for 2 min, followed by 44 cycles of denaturation at 95 °C for 5 sec, annealing at 60 °C for 30 sec, and extension at 72 °C for 1 sec. Subsequently, a melting curve analysis was performed with a denaturation step at 95 °C for 5 sec, followed by annealing at 60 °C for 1 min and gradual heating to 95 °C at a ramp-rate of 0.11 °C/s. Finally, the product was cooled to 37 °C for 3 min (Vanhauwaert *et al.*, 2014 [↗](#)). The data was analyzed using the qBase+ software (Biogazelle).

Osteoblast imaging in transgenic *osx:Kaede* larvae

Ten zebrafish larvae (at 7 dpf and 14 dpf) with the transgenic *osx:Kaede* background were anesthetized using 1x Tricaine. Imaging was performed using the Leica microscope M165FC and mounted camera (DFC450C) operated by LAS V4.3 software (Leica Microsystems, Wetzlar, Germany). Images of 7 dpf larvae were taken from the ventral side. Images of 14 dpf larvae were taken from both ventral and lateral perspectives to provide a more comprehensive view of the opercle’s surface area.

Fiji software (version 2.14.0), powered by ImageJ, was employed for all measurements (Schindelin *et al.*, 2012 [↗](#)). Osteoblast-positive area of both the total head and opercle was quantified using thresholding, followed by measurement of the positive area. All measurements were performed in triplicate on blinded pictures. The presence of osteoblasts in the opercle was measured by hand using the polygon selection tool. Mann-Whitney U test was applied in GraphPad Prism (v.9.4.0), with p-values considered significant when ≤ 0.05 .

Alizarin red staining and imaging of zebrafish larvae

The ten zebrafish larvae, that were previously used for osteoblast imaging at 7 dpf and 14 dpf, were euthanized using 25x Tricaine. They were transferred to a cell strainer and washed with dH₂O several times to remove the Tricaine. The strainers were placed in a 6-well plate and incubated in 4% PFA overnight at 4°C. The plates were sealed with parafilm to prevent evaporation. The larvae were then washed with dH₂O several times to remove the PFA and bleached for 30 minutes at room temperature using a solution containing 3% H₂O₂ and 2% KOH to remove pigmentation. Next, they were stained overnight at 4°C using Alizarin Red S (0.005% in 1% KOH/2% Triton). The samples were washed with dH₂O several times and transferred to increasing concentrations of glycerol (30-70-100% for 5 minutes each) for storage (4°C) and imaging. Zebrafish larvae stained with Alizarin red were then imaged using a Leica M165FC microscope and DFC450C camera with the LAS V4.3 software (Leica Microsystems). The ventral side of the larvae was captured at 7 dpf. Both ventral and lateral perspectives were captured at 14 dpf to provide a more comprehensive view of the opercle's surface area and the number of mineralized vertebrae.

Fiji software (version 2.14.0), powered by ImageJ, was employed for all measurements (Schindelin *et al.*, 2012 [DOI](#)). The red stain in the head elements was assessed using thresholding, followed by quantification of the positive area. These measurements were conducted in triplicate on blinded pictures. The stained notochord tip and opercle was measured by hand using the polygon selection tool. The statistical analysis employed the Mann-Whitney U test in GraphPad Prism (v.9.4.0), with p-values considered significant when ≤ 0.05 .

Micro-Computed Tomography (MicroCT) analysis in adult zebrafish

Adult zebrafish (3 months post fertilization) were euthanized using a 25x tricaine solution (4000 mg tricaine powder (Sigma), 979 ml distilled water, and 1M Tris, adjusted to pH 7). Brightfield images of the zebrafish were taken using a Leica M165FC microscope and DFC450C camera with the LAS V4.3 software (Leica Microsystems). The standard lengths of the zebrafish were measured using the Fiji (ImageJ) software (ImageJ 1.52i) (Schindelin *et al.*, 2012 [DOI](#)).

The fish were fixed for approximately one week in a fixative solution (4% paraformaldehyde, 5% triton X-100, and 1% potassium hydroxide). The solution was changed when it turned yellow. A maximum of five fish per 100 ml of fixative solution was used. After fixation, the fish were transferred to a 70% ethanol solution for storage until scanning.

Before scanning, three fish were transferred to a 15 ml Eppendorf tube and immobilized using paper towel soaked in 70% ethanol. The Eppendorf tubes were scanned at the custom-built HECTOR scanner of the Centre for X-ray Tomography (UGCT, www.ugct.ugent.be [DOI](#)). A hardware filter of 0.5 mm Al was used to eliminate beam hardening artefacts, with the tube voltage at 90 kVp and target power of 10 W. During a 360° rotation, 1201 radiographic images were acquired at 1 s acquisition time per image. The raw data was reconstructed using the Octopus Reconstruction software tool, resulting in a 3D volume of approximately 2800×1000×1000 voxels. Using geometrical magnification, a voxel size of 20³ μm³ was obtained (Masschaele *et al.*, 2013 [DOI](#)).

The 3 fish in one tube were virtually separated from the scan, aligned and exported as 3 individual single tiff volume using VGStudioMAX (VolumeGraphics, Heidelberg, Germany). The generated volumes were analyzed using the FishCut software in Matlab described in Hur *et al.*, 2017 [DOI](#). The resulting plots were generated using R statistics and were color-coded to highlight significant differences. Significant differences were represented with a lighter color scheme.

Alizarin red staining and imaging of adult zebrafish

The fish used for microCT were reused for Alizarin Red staining for which the protocol has been described in [Bek et al., 2021](#) [↗](#). In short, the fish were transferred to cassettes and the concentration of EtOH was gradually reduced from 70% to distilled water (70%-50%-30%-dH₂O each 30 min). Then, the samples were enhanced, immersed into the bone-staining medium, stained with bone-staining solution and destained after removal of the scales with destaining solution. Finally, the samples were gradually (30-70-100%) transferred to 100% glycerol for storage (4°C) and imaging.

Adult zebrafish were imaged using a Leica M165FC microscope and DFC450C camera with the LAS V4.3 software (Leica Microsystems). The DSR DsRed Dichroic Mirror filter was used to visualize the (red) fluorescent signal. Images were obtained from a lateral view to get a clear picture of the whole fish. Higher magnification was used to get detailed images of the vertebral column and the head. Images of the head were used to measure the head size, using the Fiji (ImageJ) software ([Schindelin et al., 2012](#) [↗](#)).

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Reviewer #1 (Public review):

Summary:

In this work, a screening platform is presented for rapid and cost-effective screening of candidate genes involved in Fragile Bone Disorders. The authors validate the approach of using crispants, generating FO mosaic mutants, to evaluate the function of specific target genes in this particular condition. The design of the guide RNAs is convincingly described, while the effectiveness of the method is evaluated to 60% to 92% of the respective target genes being presumably inactivated. Thus, injected FO larvae can be directly used to investigate the consequences of this inactivation.

Skeletal formation is then evaluated at 7dpf and 14dpf, first using a transgenic reporter line revealing fluorescent osteoblasts, second using alizarin-red staining of mineralized structures. In general, it appears that the osteoblast-positive areas are more often affected in the crispants compared to the mineralized areas, an observation that appears to correlate with the observed reduced expression of *bglap*, a marker for mature osteoblasts, and the increased expression of *col1a1a* in more immature osteoblasts.

Finally, the injected fish (except two lines that revealed a high mortality) are also analyzed at 90dpf, using alizarin red staining and micro-CT analysis, revealing an increased incidence of skeletal deformities in the vertebral arches, fractures, as well as vertebral fusions and compressions for all crispants except those for *daam2*. Finally, the Tissue Mineral Density (TMD) as determined by micro-CT is proposed as an important marker for investigating genes involved in osteoporosis.

Taken together, this manuscript is well presented, the data are clear and well analyzed, and the methods well described. It makes a compelling case for using the crispant technology to screen the function of candidate genes in a specific condition, as shown here for bone disorders.

Strengths:

Strengths are the clever combination of existing technologies from different fields to build a screening platform. All the required methods are comprehensively described.

Weaknesses:

One may have wished to bring one or two of the crispants to the stage of bona fide mutants, to confirm the results of the screening, however, this is done for some of the tested genes as laid out in the discussion.

Comments on latest version:

All my issues were resolved.

<https://doi.org/10.7554/eLife.100060.2.sa3>

Reviewer #2 (Public review):

Summary:

More and more genes and genetic loci are being linked to bone fragility disorders like osteoporosis and osteogenesis imperfecta through GWAS and clinical sequencing. In this

study, the authors seek to develop a pipeline for validating these new candidate genes using crispant screening in zebrafish. Candidates were selected based on GWAS bone density evidence (4 genes) or linkage to OI cases plus some aspect of bone biology (6 genes). NGS was performed on embryos injected with different gRNAs/Cas9 to confirm high mutagenic efficacy, and off-target cutting was verified to be low. Bone growth, mineralization, density, and gene expression levels were carefully measured and compared across crispants using a battery of assays at three different stages.

Strengths:

- (1) The pipeline would be straightforward to replicate in other labs, and the study could thus make a real contribution towards resolving the major bottleneck of candidate gene validation.
- (2) The study is clearly written and extensively quantified.
- (3) The discussion attempts to place the phenotypes of different crispant lines into the context of what is already known about each gene's function.
- (4) There is added value in seeing the results for the different crispant lines side by side for each assay.
- (5) Caveats to the interpretability of crispant data and limitations of their gene-focused analyses and RT-PCR assays are discussed.

Weaknesses:

- (1) The study uses only well-established methods and is strategy-driven rather than question/hypothesis-driven. This is in line with the researchers' primary goal of developing a workflow for rapid *in vivo* functional screening of candidate genes. However, this means that less attention is paid to what the results obtained for a given gene may mean regarding potential disease mechanisms, and how contradictions with prior reports of mouse or fish null mutant phenotypes might be explained.
- (2) Normalization to body size was not performed. Measurements of surface area covered by osteoblasts or mineralized bone (Fig. 1) are typically normalized to body size - especially in larvae and juvenile fish - to rule out secondary changes due to delayed or accelerated overall growth. This was not done here; the authors argue that "variations in growth were considered as part of the phenotypic outcome." This is reasonable, but because standard length was reported only for fish at 90 dpf (not significantly different in any line), the reader is not given the opportunity to consider whether earlier differences in, e.g. surface area covered by osteoblasts at 14 dpf, could be accounted for by delayed or accelerated overall growth. Images in Figure S5 were not taken at the same magnification, further confounding this effort.

Comments on latest version:

The authors have largely addressed my comments by making changes to the text.

However, in response to one of my original comments ("It would be helpful to note the grouping of candidates into OI vs. BMD GWAS throughout the figures"), they added a sentence to this effect to the legends. However, because two of the lines were larval-lethal, the legends to Figs. S6-8 are now incorrect in referring to ten genes when only eight mutants are shown.

<https://doi.org/10.7554/eLife.100060.2.sa2>

Reviewer #3 (Public review):

The manuscript describes the use of CRISPR gene editing coupled with phenotyping mosaic zebrafish larvae to characterize functions of genes implicated in heritable fragile bone disorders (FBDs). Authors targeted six high-confident candidate genes implicated in severe recessive forms of FBDs and four Osteoporosis GWAS-implicated genes and observe varied developmental phenotypes across all crispants, in addition to adult skeletal phenotypes. While the study lacks insight on underlying mechanisms that contribute to disease phenotypes, a major strength of the paper is the streamlined method that produced significant phenotypes for all candidate genes tested. It also represents a significant increase in number of candidate genes tested using their crispant approach beyond the single mutant that was previously published.

One weakness was the variability of developmental phenotypes, addressed by authors in the Discussion. This might be a product of maternal transcripts not targeted by CRISPR or genetic compensation, which authors have not fully explored. Overall, the paper was well-written and easy to read.

Comments on latest version:

The authors have addressed many concerns in this revision. Figure 1 and Table 2 are much improved.

While details of orthologous gene expression profiles of target genes is a welcome addition, other features of target genes remain unaddressed. For example, do genes with maternally deposited transcript exhibit dampened phenotypes? Or does genetic compensation impact certain genes more than others? Since authors state that the study represents a methods paper, it will be important for users to understand the caveats of gene selection to effectively implement and interpret results of the approach.

<https://doi.org/10.7554/eLife.100060.2.sa1>

Author response:

The following is the authors' response to the original reviews.

Public Reviews:

Reviewer #1 (Public review):

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In this work, a screening platform is presented for rapid and cost-effective screening of candidate genes involved in Fragile Bone Disorders. The authors validate the approach of using crispants, generating FO mosaic mutants, to evaluate the function of specific target genes in this particular condition. The design of the guide RNAs is convincingly described, while the effectiveness of the method is evaluated to 60% to 92% of the respective target genes being presumably inactivated. Thus, injected FO larvae can be directly used to investigate the consequences of this inactivation.

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mature osteoblasts, and the increased expression of col1a1a in more immature osteoblasts.

Finally, the injected fish (except two lines that revealed high mortality) are also analyzed at 90dpf, using alizarin red staining and micro-CT analysis, revealing an increased incidence of skeletal deformities in the vertebral arches, fractures, as well as vertebral fusions and compressions for all crispants except those for daam2. Finally, the Tissue Mineral Density (TMD) as determined by micro-CT is proposed as an important marker for investigating genes involved in osteoporosis.

Taken together, this manuscript is well presented, the data are clear and well analyzed, and the methods are well described. It makes a compelling case for using the crispant technology to screen the function of candidate genes in a specific condition, as shown here for bone disorders.

Strengths:

Strengths are the clever combination of existing technologies from different fields to build a screening platform. All the required methods are comprehensively described.

We would like to thank the reviewer for highlighting the strengths of our paper.

Weaknesses:

One may have wished to bring one or two of the crispants to the stage of bona fide mutants, to confirm the results of the screening, however, this is done for some of the tested genes as laid out in the discussion.

We thank the reviewer for their comment. We would like to point out that indeed similar phenotypes have been observed in existing models, as mentioned in the discussion section.

Reviewer #2 (Public review):

Summary:

More and more genes and genetic loci are being linked to bone fragility disorders like osteoporosis and osteogenesis imperfecta through GWAS and clinical sequencing. In this study, the authors seek to develop a pipeline for validating these new candidate genes using crispant screening in zebrafish. Candidates were selected based on GWAS bone density evidence (4 genes) or linkage to OI cases plus some aspect of bone biology (6 genes). NGS was performed on embryos injected with different gRNAs/Cas9 to confirm high mutagenic efficacy and off-target cutting was verified to be low. Bone growth, mineralization, density, and gene expression levels were carefully measured and compared across crispants using a battery of assays at three different stages.

Strengths:

(1) The pipeline would be straightforward to replicate in other labs, and the study could thus make a real contribution towards resolving the major bottleneck of candidate gene validation.

(2) The study is clearly written and extensively quantified.

(3) The discussion attempts to place the phenotypes of different crispant lines into the context of what is already known about each gene's function.

(4) *There is added value in seeing the results for the different crispant lines side by side for each assay.*

We would like to thank the reviewer for highlighting the strengths of our paper.

Weaknesses:

(1) *The study uses only well-established methods and is strategy-driven rather than question/hypothesis-driven.*

We thank the reviewer for this correct remark. The mayor aim of this study was to establish a workflow for rapid *in vivo* functional screening of candidate genes across a broad range of FBDs.

(2) *Some of the measurements are inadequately normalized and not as specific to bone as suggested:*

(a) *The measurements of surface area covered by osteoblasts or mineralized bone (Figure 1) should be normalized to body size. The authors note that such measures provide "insight into the formation of new skeletal tissue during early development" and reflect "the quantity of osteoblasts within a given structure and [is] a measure of the formation of bone matrix." I agree in principle, but these measures are also secondarily impacted by the overall growth and health of the larva. The surface area data are normalized to the control but not to the size/length of each fish - the *esr1* line in particular appears quite developmentally advanced in some of the images shown, which could easily explain the larger bone areas. The fact that the images in Figure S5 were not all taken at the same magnification further complicates this interpretation.*

We thank the reviewer for this detailed and insightful remark. We agree with the reviewer and recognize that the results may be influenced by size differences. However, we do not normalize for size, as variations in growth were considered as part of the phenotypic outcome. This consideration has been addressed in the discussion section.

Line 335-338: 'Although the measurements of osteoblast-positive and mineralized surface areas may be influenced by size differences among some of the crispants, normalization to size parameters was not conducted, as variations in growth were considered integral to the phenotypic outcome.'

Line 369: 'Phenotypic variability in these zebrafish larvae can be attributed to several factors, including crispant mosaicism, allele heterogeneity, environmental factors, differences in genomic background **and development**, and slightly variable imaging positioning.'

(b) *Some of the genes evaluated by RT-PCR in Figure 2 are expressed in other tissues in addition to bone (as are the candidate genes themselves); because whole-body samples were used for these assays, there is a nonzero possibility that observed changes may be rooted in other, non-skeletal cell types.*

We thank the reviewer for this valuable comment. We acknowledge that the genes assessed by RT-PCR are expressed in other tissues beyond bone. This consideration has been addressed in the discussion section.

Line 362-365: "However, it is important to note that the genes evaluated by RT-PCR are not exclusively expressed in bone tissue. Since whole-body samples were used for expression analysis, there is a possibility that the observed changes in gene expression may be influenced by other non-skeletal cell types".

(3) Though the assays evaluate bone development and quality at several levels, it is still difficult to synthesize all the results for a given gene into a coherent model of its requirement.

We appreciate the reviewer's remark. We acknowledge that the results for the larval stages exhibit variability, making it challenging to synthesize them into a coherent model. However, it is important to emphasize that all adult crispant consistently display a skeletal phenotype. Consequently, the feasibility and reproducibility of this screening method are primarily focusing on the adult stages. This consideration has been addressed in the discussion section of the manuscript.

Line 391-399: 'In adult crispants, the skeletal phenotype was generally more penetrant. All crispants showed malformed arches, a majority displayed vertebral fractures and fusions and some crispants exhibited distinct quantitative variations in vertebral body measurements. This confirmed the role of the selected genes in skeletal development and homeostasis and their involvement in skeletal disease and established the crispant approach as a valid approach for rapidly providing in vivo gene function data to support candidate gene identification.'

(4) Several additional caveats to crispant analyses are worth noting:

(a) False negatives, i.e. individual fish may not carry many (or any!) mutant alleles. The crispant individuals used for most assays here were not directly genotyped, and no control appears to have been used to confirm successful injection. The authors therefore cannot rule out that some individuals were not, in fact, mutagenized at the loci of interest, potentially due to human error. While this doesn't invalidate the results, it is worth acknowledging the limitation.

We thank the reviewer for this valuable remark. We recognize the fact that working with crispants has certain limitations, including the possibility that some individuals may carry few or no mutant alleles. To address this issue, we use 10 individual crispants during the larval stage and 5 during the adult stage. Although some individuals may lack the mutant alleles, using multiple fish helps reduce the risk of false negatives.

Furthermore, we perform NGS analysis on pools of 10 embryos from the same injection clutch as the fish used in the various assays to assess the indel efficiency. While there remains a possibility of false negatives, the overall indel efficiency, as indicated by our NGS analysis, is high (>90%), thereby reducing the likelihood of having crispants with very low indel efficiency. We included this in the discussion.

Line 387-390: 'While there remains a possibility of false negatives, the overall indel efficiency, as indicated by our NGS analysis, is high (>90%), thereby reducing the likelihood of having crispants with very low indel efficiency.'

(b) Many/most loci identified through GWAS are non-coding and not easily associated with a nearby gene. The authors should discuss whether their coding gene-focused pipeline could be applied in such cases and how that might work.

The authors thank the reviewer for this insightful comment. Our study is focused on strong candidate genes rather than non-coding variants. We recognize that the use of this workflow poses challenges for analyzing non-coding variants, which represents a limitation of the crispant approach. We have addressed this issue in the discussion section of the manuscript.

Line 131: 'Gene-based'

Line 453: 'Gene-based'

Line 311-314: 'It is important to note that this study focused on candidate genes for osteoporosis, not on the role of specific variants identified in GWAS studies. Non-coding variants for instance, which are often identified in GWAS studies, present significant challenges in terms of functional validation and interpretation.'

Reviewer #3 (Public review):

Summary:

The manuscript "Crispant analysis in zebrafish as a tool for rapid functional screening of disease-causing genes for bone fragility" describes the use of CRISPR gene editing coupled with phenotyping mosaic zebrafish larvae to characterize functions of genes implicated in heritable fragile bone disorders (FBDs). The authors targeted six high-confident candidate genes implicated in severe recessive forms of FBDs and four Osteoporosis GWAS-implicated genes and observed varied developmental phenotypes across all crispants, in addition to adult skeletal phenotypes.

A major strength of the paper is the streamlined method that produced significant phenotypes for all candidate genes tested.

We would like to thank the reviewer for highlighting the strengths of our paper.

A major weakness is a lack of new insights into underlying mechanisms that may contribute to disease phenotypes, nor any clear commonalities across gene sets. This was most evident in the qRT-PCR analysis of select skeletal developmental genes, which all showed varied changes in fold and direction, but with little insight into the implications of the results.

We thank the reviewer for this insightful remark. We want to emphasize that this study focusses on establishing a new screening method for candidate genes involved in FBDs, rather than investigating the underlying mechanisms contributing to disease phenotypes. However, to investigate the underlying mechanisms in these crispants, the creation of bona fide mutants is necessary. We have included this consideration in the discussion.

Furthermore, we acknowledge that the results for the larval stages exhibit variability, which can complicate the interpretation of these findings. This is particularly true for the RT-PCR analysis, where whole-body samples were used, raising the possibility that other tissues may influence the expression results. Therefore, our primary focus is on the adult stages, as all crispants display a skeletal phenotype at this age. We have elaborated on this point in the discussion.

Line 462-463: 'Moreover, to explore the underlying mechanisms contributing to disease phenotypes, it is essential to establish stable knockout mutants derived from the crispants'.

Line 391-399: 'In adult crispants, the skeletal phenotype was generally more penetrant. All crispants showed malformed arches, a majority displayed vertebral fractures and fusions and some crispants exhibited distinct quantitative variations in vertebral body measurements. This confirmed the role of the selected genes in skeletal development and homeostasis and their involvement in skeletal disease and established the crispant approach as a valid approach for rapidly providing in vivo gene function data to support candidate gene identification.'

Ultimately, the authors were able to show their approach is capable of connecting candidate genes with perturbation of skeletal phenotypes. It was surprising that all four

GWAS candidate genes (which presumably were lower confidence) also produced a result.

We appreciate the reviewer's comment. We would like to direct attention to the discussion section, where we offer a possible explanation for the observation that all four GWAS candidate genes produce a skeletal phenotype.

Line 460-410: 'The more pronounced and earlier phenotypes in these zebrafish crispants are most likely attributed to the quasi knock-out state of the studied genes, while more common less impactful variants in the same genes result in typical late-onset osteoporosis (Laine et al., 2013) . This phenomenon is also observed in knock-out mouse models for these genes (Melville et al., 2014)(Coughlin et al., 2019).'

These authors have previously demonstrated that crispants recapitulate skeletal phenotypes of stable mutant lines for a single gene, somewhat reducing the novelty of the study.

We thank the reviewer for this comment and appreciate their concern. We have indeed demonstrated that crispants can recapitulate the skeletal phenotypes observed in stable mutant lines for the osteoporosis gene LRP5. However, we would like to highlight that the current study represents the first large-scale screening of candidate genes associated with bone disorders, including genes related to both OI and osteoporosis. We have included this information in both the abstract and the discussion

Line 60-62: 'We advocate for a novel comprehensive approach that integrates various techniques and evaluates distinct skeletal and molecular profiles across different developmental and adult stages.'

Line 456-457: 'While this work represents a pioneering effort in establishing a screening platform for skeletal diseases, it offers opportunities for future improvement and refinement.'

Recommendations for the authors:

Reviewer #1 (Recommendations for the authors):

(1) Figure 1a: what does the differential shading of the bone elements represent? Explain in the legend.

The differential shading doesn't represent anything specific. It's simply used to enhance the visual appeal and to help distinguish between the different structures. We removed the shading in the figure.

(2) Supplementary Figures 2-5: should the numbering of these figures be also in order of appearance in the text? I understand that the authors prefer to associate the transgenic and the alizarin red-stained specimens, however, the reading would be easier that way.

We changed this accordingly.

(3) Lines 275-276: "no significant differences in standard length (Figure 4a)": should be Figure 4b.

The suggested changes are incorporated in the manuscript.

Line 276-277: 'Among the eight crispants that successfully matured into adulthood, none exhibited significant differences in standard length and head size (n=5 fish per crispant)

(Figure 4b).’

(4) Line 277 "larger eye diameter": should be Figure 4b.

The suggested changes are incorporated in the manuscript.

Line 378: ‘However, *esr1* crispants were observed to have notably larger eye diameters (Figure 4b).’

(5) Line 280: "no obvious abnormalities were detected (Figure 4b,c)": should be Figure 4a, c. Note that the authors may reconsider the a, b, c numbering in Figure 4 by inverting a and b.

The suggested changes are incorporated in the manuscript.

Line 278-281: ‘All these crispants demonstrated various abnormalities in the caudal part of the vertebral column such as fusions, compressions, fractures, or arch malformations, except for *daam2* crispants where no obvious abnormalities were detected (Figure 4a,c; Supplementary Figure 6).’

(6) Table 2: This table, which recapitulates all the results presented in the manuscript, is in the end the centerpiece of the work. It is however difficult to read in its present form. Three suggestions:

- Transpose it such that each gene has its own column, and the lines give the results for the different measurements
- Place the measurements that result in "ns" for all crispants at the end (bottom) of the table.
- Maybe bring the measurements at 7dpf, 14dpf, and 90 dpf together.

We agree with the reviewer and have added a new table where we transposed the data. However, we chose not to place the measurements that resulted in 'ns' for all crispants at the end of the table, as we believe it is important to track the evolution of the phenotype over time. Where possible, we have grouped the measurements for 7 dpf and 14 dpf together.

Reviewer #2 (Recommendations for the authors):

(1) It would help to justify why these particular area measurements are appropriate for this set of candidate genes, which were selected based on putative links to bone quality rather than bone development.

The selected methods are among the most commonly used to evaluate bone phenotypes. They are straightforward to reproduce, as well as cost- and time-effective. The strength of this approach lies in its use of simple, reproducible techniques that form the foundation for characterizing bone development. Although the candidate genes were chosen based on their putative links to bone quality, early skeletal phenotypes can already be observed during bone development.

The mineralized surface area of the total head and specific head structures was selected to evaluate the degree of mineralization in early skeletal development, as mineralization is a direct indicator of bone formation. Additionally, the osteoblast-positive surface areas were measured to provide insight into the formation of new skeletal tissue during early development. Osteoblasts, as active bone-forming cells, are essential for understanding bone growth and the dynamics of skeletal phenotypes.

Examples in the manuscript:

Line 212-214: ‘The osteoblast-positive areas in both the total head and the opercle were then quantified to gain insight into the formation of new skeletal tissue during early development.’

Line 221-223: ‘Subsequently, Alizarin Red S (ARS) staining was conducted on the same 7 and 14 dpf crispant zebrafish larvae in order to evaluate the degree of mineralization in the early skeletal structures.’

(2) Reword: The opercle bone is the earliest forming bone of the opercular series, and appears to be what the authors are referring to as the "operculum" at 7-14 dpf. The operculum is the larger structure (gill cover) in which the opercle is embedded. It would be more accurate to simply refer to the opercle at these stages.

We agree with this comment and changed the text accordingly.

(3) Define BMD and TMD at first usage.

BMD and TMD are now defined in the manuscript.

Line 41-43: ‘Six genes associated with severe recessive forms of Osteogenesis Imperfecta (OI) and four genes associated with bone mineral density (BMD), a key osteoporosis indicator, identified through genome-wide association studies (GWAS) were selected.’

Line 286-288: ‘For each of the vertebral centra, the length, tissue mineral density (TMD), volume, and thickness were determined and tested for statistical differences between groups using a regression-based statistical test (Supplementary Figure 7).’

(4) It would be helpful to note the grouping of candidates into OI vs. BMD GWAS throughout the figures.

We agree with this comment and added this to all figure legends.

‘The first four genes are associated with the pathogenesis of osteoporosis, while the last six are linked to osteogenesis imperfecta’

Reviewer #3 (Recommendations for the authors):

Major points:

(1) For the Results, it would be useful to the Reader to justify the selection of human candidate genes and their associated zebrafish orthologs to model skeletal functions. For example, what are variants identified from human studies, and do they impact functional domains? Are these domains and/or proteins conserved between humans/zebrafish? Is there evidence of skeletal expression in humans/zebrafish?

Supplementary Table 4 lists the selected human candidate genes with reported mutations and/or polymorphisms associated with both skeletal and non-skeletal phenotypes. The table also includes additional findings from studies in mice and zebrafish. An extra column was now added to indicate gene conservation between human and zebrafish. We consulted UniProt (<https://www.uniprot.org>) and ZFIN (<https://zfin.org>) to assess the skeletal expression of these genes in human and zebrafish. All genes showed expression in the trabecular bone and/or bone marrow in humans, as well as in bone elements in zebrafish. We added this in the discussion.

Line 309: ‘All selected genes show skeletal expression in both human and zebrafish.’

Supplemental table 4 legend: ‘The conservation between human and zebrafish is reported in the last column.’

As part of this, some version of Supplementary Table 4 might be included as a main display to introduce the targeted genes, ideally separated by rare (recessive OI) vs. common disease (osteoporosis). In the case of common disease and GWAS hits, how did authors narrow in on candidate genes (which often have Mbp-scale associated regions spanning multiple genes)? Further, what is the evidence that the mechanism of action of the GWAS variant is haploinsufficiency modeled by their crispant zebrafish?

We have kept Supplementary Table 4 in the supplementary material but have referred to it earlier in the manuscript’s introduction. Consequently, the table has been renumbered from ‘Supplementary Table 4’ to ‘Supplementary Table 1’.

The selection of genes potentially involved in the pathogenesis of osteoporosis is based on the data from the GWAS catalog, which annotates SNPs using the Ensemble mapping pipeline. The available annotation on their online search interface includes any Ensemble genes to which a SNP maps, or the closest upstream and downstream gene within a 50kb window. Four genes were selected for this screening method based on the criteria outlined in the results section. In this study, we aim to evaluate the general involvement of specific genes in bone metabolism, rather than to model a specific variant.

Line 135-136 and 309-311: ‘An overview of the selected genes with observed mutant phenotypes in human, mice and zebrafish is provided in Supplementary Table 1.’

(2) Using the crispant approach does not impact maternally-deposited RNAs that would dampen early developmental phenotypes. Considering the higher variability in larval phenotypes, perhaps the maternal effect plays a role. The authors might investigate developmental expression profiles of their genes using existing RNA-seq datasets such as from White et al (doi: 10.7554/eLife.30860).

We thank the reviewer for this comment and agree with the possibility that maternally-deposited RNAs might have an impact on early developmental phenotypes. We included this in the discussion.

Line 369-372: ‘Phenotypic variability in these zebrafish larvae can be attributed to several factors, including crispant mosaicism, allele heterogeneity, environmental factors, differences in genomic background and development, maternally-deposited RNAs, and slightly variable imaging positioning.’

(3) While making comparisons within a clutch of mutant vs scrambled control is crucial, it is also important to ensure phenotypes are not specific to a single clutch. Do phenotypes remain consistent across different crosses/clutches?

Yes, phenotypes remain consistent across different crosses and clutches. We included images from a second clutch in the Supplementary material (Supplementary Figure 8) and referred to it in the discussion.

Line 394-397: ‘Additionally, these skeletal malformations were consistently observed in a second clutch of crispants (Supplementary Figure 8), underscoring the reproducibility of these phenotypic features across independent clutches.’

(4) Understanding that antibodies may not exist for many of the selected genes for zebrafish, authors should verify haploinsufficiency using an RT-qPCR of targeted genes in crispants vs. controls.

We appreciate the reviewer's suggestion to use RT-qPCR to examine expression levels of the targeted genes in crispants. However, previous experience suggests that relying on RNA expression to verify haploinsufficiency in zebrafish can be challenging. In zebrafish KO mutants, RT-qPCR often still detects gene transcripts, potentially due to incomplete nonsense-mediated decay (NMD) of the mutated mRNA, which may allow residual expression even in the absence of functional protein. As a more definitive approach, we prefer to use antibodies to confirm haploinsufficiency at the protein level. However, as the reviewer noted, generating and applying specific antibodies in zebrafish remains challenging.

(5) Please indicate how parametric vs. non-parametric statistical tests were selected for datasets.

We initially selected the parametric unpaired t-test, assuming the data were normally distributed with similar variances between groups. We verified the assumption of equal variances using the F-test, which was not significant across all assays. However, we did not assess the normality of the data directly, meaning we cannot confirm the normality assumption required for the t-test. Given this, we have opted to use the non-parametric Mann-Whitney U test, which does not require assumptions of normality, to ensure the robustness of our statistical analyses. We changed the Figures, the figure legends and the text accordingly.

(6) In the figures and tables, I recommend adding notation showing the grouping of the first four genes as GWAS osteoporosis, the next three genes as osteoblast differentiation, the next two genes as bone mineralization, and the final gene as collagen transport to orient the reader. One might expect there to be a clustering of phenotypic outcomes based on the selection of genes, and it would be easier to follow this. This would be particularly useful to include in Table 2.

Our primary objective is to assess the feasibility and reproducibility of the crispant screen rather than performing an in-depth pathway analysis or categorizing genes by biological processes. For this purpose, we have organized candidate genes based on their relevance to osteoporosis and Osteogenesis Imperfecta, without subdividing them further. We have clarified this focus in the figure legends, as suggested in an earlier recommendation.

(7) For Figure 1, consider adding a smaller zoomed version of 1a embedded in each sub-figure with each measured element highlighted to improve readability.

We agree with this comment and changed the figure accordingly.

Minor points:

(1) Table 2 could be simplified to improve readability. The headers have redundancies across columns with varied time points and could be merged.

The suggested changes are incorporated in the manuscript (see earlier comment about this).

(2) "BMD" is not defined in the Abstract. This is a personal preference, but there were numerous abbreviations in the text that made it difficult to follow at times.

The suggested changes are incorporated in the manuscript (see earlier comment about this).

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