

## Resource

# OutKnocker: a web tool for rapid and simple genotyping of designer nuclease edited cell lines

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The application of designer nucleases allows the induction of DNA double-strand breaks (DSBs) at user-defined genomic loci. Due to imperfect DNA repair mechanisms, DSBs can lead to alterations in the genomic architecture, such as the disruption of the reading frame of a critical exon. This can be exploited to generate somatic knockout cell lines. While high genome editing activities can be achieved in various cellular systems, obtaining cell clones that contain all-allelic frameshift mutations at the target locus of interest remains a laborious task. To this end, we have developed an easy-to-follow deep sequencing workflow and the evaluation tool OutKnocker ([www.OutKnocker.org](http://www.OutKnocker.org)), which allows convenient, reliable, and cost-effective identification of knockout cell lines.

[Supplemental material is available for this article.]

Advances in targeted genome editing technologies have opened new avenues for addressing challenging questions in the field of life sciences. The recent introduction of designer nucleases such as ZFNs (Carroll 2011), TALENs (Miller et al. 2011), or CRISPR/Cas systems (Jinek et al. 2012; Cong et al. 2013; Mali et al. 2013) allows for highly efficient, flexible, and specific induction of DNA double-strand breaks (DSB) in eukaryotic genomes. DSBs trigger two distinct repair pathways that can be exploited to specifically modify gene architecture (Carroll 2011). While the process of homologous recombination (HR) accurately repairs DSBs using the sister chromatid as a template, nonhomologous end-joining (NHEJ) repair is an error-prone end-joining mismatch repair pathway that frequently leads to genetic alterations (Lieber 2010; Chiruvella et al. 2013). Providing a donor construct with appropriate homology arms as a template, the pathway of DSB-triggered HR can be used to site-specifically introduce heterologous genetic material into cells (Carroll 2011). For example, it is possible to generate gene knockouts in somatic cell lines by introducing marker cassettes with premature stop codons. However, this strategy is time consuming and laborious and therefore not optimal for high-throughput approaches. The DSB-induced NHEJ repair pathway, on the other hand, leads to insertions or deletions (indels) (Lieber 2010) that can result in frameshift mutations and thus loss-of-function phenotypes if located within early coding exons.

While in HR-based genome editing approaches marker genes can be introduced to select for the desired genotype starting from a polyclonal cell culture, frameshift mutations induced by NHEJ are difficult to select for unless the editing event provides a survival benefit. To this end, single-cell cloning and subsequent sequencing of the genetic locus is required to obtain cells with the desired gene disruption. Sanger sequencing is most commonly used to identify modified alleles. However, in addition to being costly, this method requires a locus-specific PCR to be subcloned in order to sequence single alleles, and thus is not practical for large-scale projects. Moreover, the ploidy of the genome may vary between

cell lines and even between loci, which may require the sequencing of a considerable number of PCR subclones to reliably identify cell clones with all-allelic frameshift mutations. Small benchtop deep sequencing machines can achieve a far greater throughput. Theoretically, even low sequencing capacities are sufficient to analyze hundreds of clones in parallel, without the need to subclone PCR products. However, analysis of deep sequencing data remains challenging and no streamlined workflow has been described that would allow full exploitation of deep sequencing capacities in gene disruption projects.

Here we describe OutKnocker, a web-based application that facilitates the analysis of deep sequencing data to identify knockout cells obtained from designer nuclease-mediated genome editing. We aimed at developing an evaluation tool to genotype single-cell clones at a confined genomic region for indel mutations, as they are typically induced by designer nuclease targeting. As such, we established an algorithm that focuses on identifying a single indel event per sequencing read around a predefined target site, while ignoring SNPs or point mutations originated during sequencing. Optionally, our software also allows the detection of specific point mutations introduced by targeted mutagenesis. To fully exploit sequencing capacities, OutKnocker was designed to analyze data of sequencing runs that have been multiplexed to evaluate the same or different genomic target regions in parallel, while only requiring a limited number of unidirectional sequencing reads. OutKnocker is operated from a web browser making it conveniently accessible to any user.

## Results

### OutKnocker deep sequencing analysis tool

The graphic user interface of OutKnocker retrieves the genomic reference locus and the nuclease target site from the user (Supplemental

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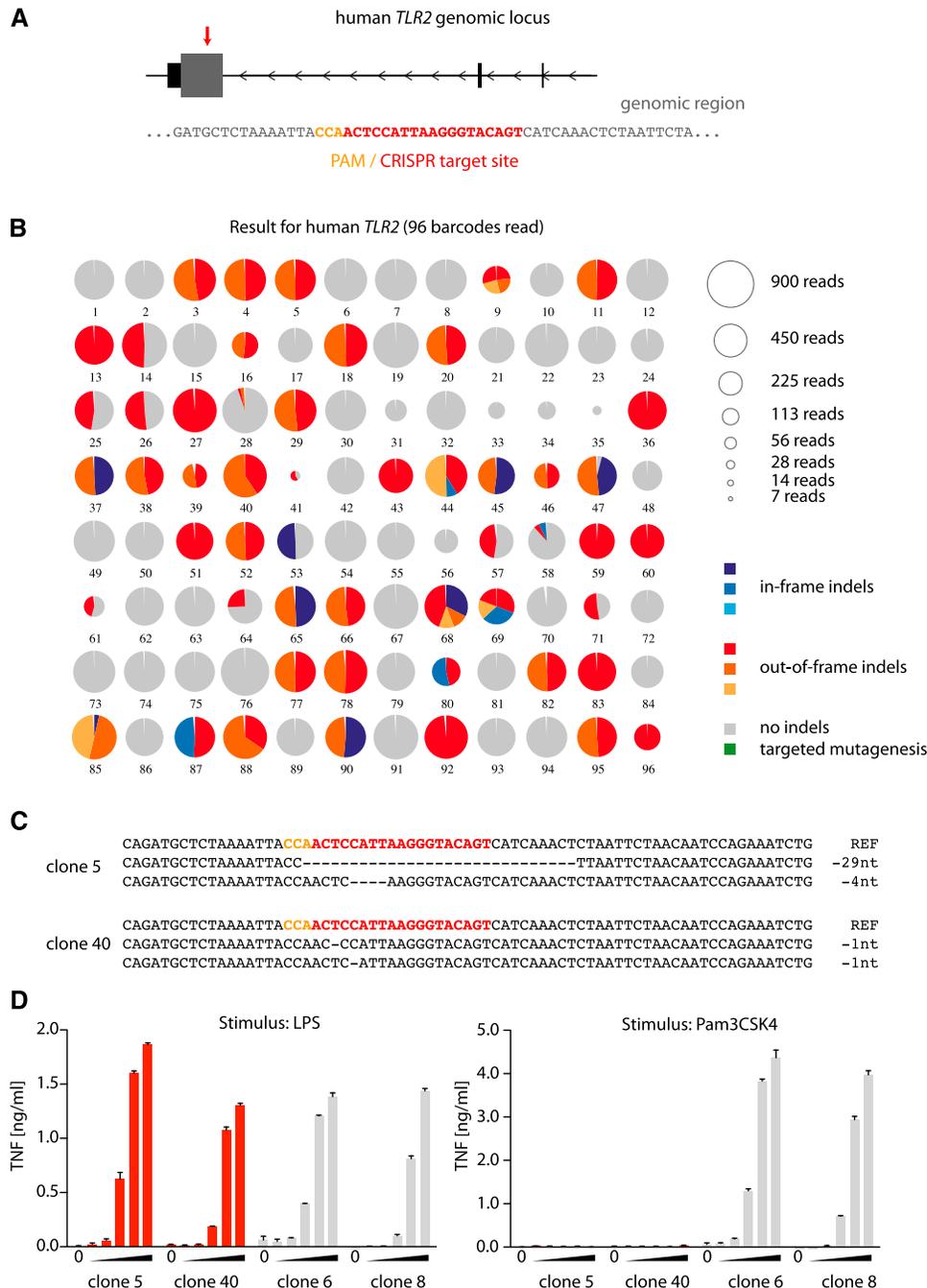
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## Validation of the OutKnocker tool

To validate this analysis tool, we targeted the toll-like receptor 2 (*TLR2*) and unc-93 homolog B1 (*C. elegans*) (*UNC93B1*) genes in

the human monocyte-like cell line THP-1 (Fig. 2A; Supplemental Fig. 3A). *TLR2* is involved in the recognition of bacterial cell wall components (Aliprantis et al. 1999), whereas *UNC93B1* is an ER-resident trafficking molecule that is essential for the function of



**Figure 2.** Application of the OutKnocker analysis tool to generate *TLR2* knockout THP-1 cells. (A) The genomic locus of the human *TLR2* gene is depicted. Small, black square represents noncoding exons, whereas the large, gray square represents coding exons. The red arrow highlights the target site of the CRISPR that is magnified below. (B) Shown is the analysis performed by OutKnocker of 96 THP-1 clones that were treated with a CRISPR targeting human *TLR2*. Every pie chart represents a clone, whereas the size of each chart corresponds to the number of reads that were analyzed to evaluate the clone (see legend in the top right). Colors of the individual pie areas indicate in-frame mutations (blue), out-of-frame mutations (red), or no indel calls (gray) (see legend in the bottom right). (C) The identified indel mutations of two knockout clones (5 and 40) are depicted. Orange letters highlight the PAM sequence and red letters indicate the CRISPR target site. (D) Two knockout clones (clones 5 and 40) as well as two unmodified clones (clones 6 and 8) were stimulated with increasing amounts of either the TLR4 ligand LPS (serial dilutions 1:10 from 1  $\mu$ g/mL to 0.1 ng/mL) or with the TLR2 ligand Pam3CSK4 (serial dilutions 1:10 from 1  $\mu$ g/mL to 0.1 ng/mL). A representative result out of two independent experiments is depicted as mean value + SEM of biological duplicates.

endosomal TLRs (Tabeta et al. 2006). To this end, CRISPR target sites were chosen to disrupt the reading frame of the respective genes in close proximity to their start codons. THP-1 cells were electroporated with a construct containing CMV-mCherry-Cas9 and an U6-gRNA cassette, and cells expressing high levels of mCherry-Cas9 were sorted and subsequently plated under limiting dilution conditions. After 2 wk, single-cell clones were selected and duplicated into new culture vessels, and one replicate was used for PCR genotyping. In a first PCR, the targeted genomic locus was amplified, and in a second PCR, barcodes and adapter sequences for Illumina deep sequencing were added. All PCR amplicons were pooled and subjected to deep sequencing (Fig. 1A). OutKnocker was then used to analyze the sequencing data for each target region individually. In total, we analyzed 96 clones for *TLR2* (Fig. 2B) and 33 clones for *UNC93B1* (Supplemental Fig. 3B) genome editing. A total of 52 out of 96 clones for *TLR2* and eight out of 33 clones for *UNC93B* displayed at least one edited allele. For the majority of clones, two distinct edited regions with roughly equal frequency could be identified, which can be interpreted as two edited alleles. However, we also detected clones that contain only one specific mutation (Fig. 2B, e.g., clones 13, 27, 36), which could be due to the fact that either all alleles bear the same indel mutation or that the clone lost one allele, which cannot be distinguished by sequencing. Data displaying more than two distinct edited sequences (Fig. 2B, clone 9) were most likely derived from two or more clones growing in a single well despite limiting dilution. At the same time, this could also be due to prolonged Cas9-mediated genome-editing activity during clonal expansion of the cells. In total, 30 of 96 (*TLR2*) and two of 33 clones (*UNC93B1*) carried frameshift mutations in all uniquely identified genomic regions (pie charts all in red color), thus representing functional knockout clones.

To confirm these genotyping results, selected clones were expanded and stimulated with TLR ligands, measuring TNF production as a readout for TLR-induced signaling. THP-1 cells were either treated with the synthetic triacylated lipopeptide Pam3CSK4, a classical TLR2 stimulus, or with the TLR4 agonist lipopolysaccharide (LPS) as a control. As expected, clones recovered with *TLR2* frameshift mutations (clones 5 and 40) showed no response to Pam3CSK4, whereas unmodified clones (clones 6 and 8) secreted TNF in a dose-dependent manner (Fig. 2C,D). As a control, all clones showed a dose-dependent response to TLR4 stimulation. Analogous data were obtained for *UNC93B1* (Supplemental Fig. 3C,D). In addition to the target regions shown here (*TLR2* and *UNC93B1*), we have generated knockout cell lines for more than 100 independent genes to date using this approach (Ablasser et al. 2013, 2014; Zhu et al. 2014; data not shown). Of note, in the case of previously characterized target genes, the phenotype of these knockout cell lines always reflected the expected outcome.

## Discussion

Here we describe an easy-to-follow workflow to genotype functional knockout or base-specifically mutated cell clones by utilizing a web browser-based evaluation tool for deep sequencing data. The data evaluation algorithm was implemented in javascript, which allows researchers to conveniently run the tool as a platform-independent service with an intuitive graphic user interface and without the requirement for transferring large amounts of data to a web server. The genotyping algorithm was streamlined for frame-disrupting allele identification while ignoring SNPs and sequencing errors typically observed with deep sequencing. This approach allows maximum information yield from limited read

numbers. However, we also included the option to identify specific point mutations introduced by targeted mutagenesis. With the setup described here, thousands of cell clones can be multiplexed in a benchtop deep sequencing run (e.g.,  $15 \times 10^6$  250-bp reads), rendering the per-clone sequencing cost below 10 cents.

## Methods

### THP-1 cell culture

THP-1 cells were cultivated at 37° and 5% CO<sub>2</sub> in RPMI supplemented with 10% FCS, 1 mM sodium pyruvate, and 0.1 mg/L Ciprofloxacin. For differentiation, cells were seeded overnight in complete medium containing 100 nM PMA. On the next day cells were washed with PBS, and seeded in flat-bottom 96-well plates at a density of  $5 \times 10^5$ /mL. Once attached, cells were stimulated with LPS (serial dilutions 1:10 from 1 µg/mL to 0.1 ng/mL), Pam3CSK4 (serial dilutions 1:10 from 1 µg/mL to 0.1 ng/mL), or R848 (serial dilutions 1:2 from 10 to 0.04 µg/mL).

### CRISPR constructs

We used a plasmid encoding a CMV-mCherry-Cas9 expression cassette and a gRNA under the U6 promoter (Ablasser et al. 2013). The CRISPR target sites used were GACTGTACCCCTTAATGGAGTTGG (*TLR2*) and GCACGTTCTTGAGCACGCCAGG (*UNC93B1*).

### Primer design

A genomic amplicon of 220- to 270-nt length was chosen with the nuclease target site located in the middle. Primers of 23 nt each with a GC content of ~50% within the entire primer sequence and a GC content of exactly 50% in the two 3'-terminal primer positions were chosen. The primer sequences were elongated by the following sequences: Fwd: ACACTCTTTCCCTACACGACGctcttccgatct - N<sub>23</sub> and Rev: TGACTGGAGTTCAGACGTGTGctcttccgatct - N<sub>23</sub>.

### Electroporation

THP-1 cells were plated at a density of  $2 \times 10^5$ /mL. After 24 h,  $2.5 \times 10^6$  cells were resuspended in 250 µL Opti-MEM, mixed with 5 µg plasmid DNA in a 4-mm cuvette, and electroporated using an exponential pulse at 250 V and 950 µF utilizing a Gene Pulser electroporating device (Bio-Rad Laboratories). Cells were allowed to recover for 2 d in 6-well plates filled with 4 mL medium per well.

### FACS sorting

FACS sorting of 20,000 mCherry-positive cells was performed on a BD FACSAria III (BD Biosciences) sorting device.

### Limiting dilution cloning

Cells were plated at a density of 4, 8, or 16 cells per well of nine round-bottom 96-well plates and grown for 2 wk. Then, plates were scanned for absorption at 600 nm. Growing clones were identified using custom software and picked and duplicated by a Biomek FXp (Beckman Coulter) liquid handling system.

### Cell lysis

The medium was discarded and the cells were lysed in 30 µL of lysis buffer: 0.2 mg/mL proteinase K, 1 mM CaCl<sub>2</sub>, 3 mM MgCl<sub>2</sub>, 1 mM

EDTA, 1% Triton X-100, 10 mM Tris (pH 7.5). The reactions were incubated for 10 min at 65°C and 15 min at 95°C.

### Dual PCR barcoding

First-level PCR reactions were performed using 1  $\mu$ L PCR-compatible lysate as a template for a 6.25- $\mu$ L Phusion (Thermo Scientific) PCR reaction according to the manufacturer's protocol (annealing temperature: 60°C; elongation time: 15 sec, 19 cycles). Of this reaction, 1  $\mu$ L was transferred to a second-level PCR using the same cycling conditions and a combination of barcode primers that is unique for each clone to be analyzed. For all primer sequences see Supplemental Table 1.

### Deep sequencing

Crude PCR products were pooled and size-separated using a 1.5% agarose gel run at 100 V. After visualization with ethidium bromide under UV light, DNA bands from 300 bp to 450 bp were cut out and purified using Jena Analytik innuPREP gel extraction kit according to the manufacturer's protocol. Eluted DNA was precipitated by adding 0.1 volumes of 3 M NaOAc (pH 5.2) and 1.1 volumes of isopropanol. After centrifugation for 15 min at 4°C, the resulting pellets were washed once in 70% EtOH and air-dried. A total of 30  $\mu$ L water was added, nonsoluble fractions were spun down and removed, and the DNA concentration was quantified using a Nanodrop spectrophotometer system (Thermo Fisher). Deep sequencing was performed according to the manufacturer's protocol using the MiSeq (Illumina) benchtop sequencing system. Data were obtained in FASTQ format.

### Data evaluation

Data evaluation by OutKnocker was performed using an Apple MacBook Pro (2.3 GHz Dual-Core, 4 GB RAM) on Firefox version 27.0.1. OutKnocker also runs on current versions of Safari and Google Chrome.

### Data access

The sequence data generated for this study have been submitted to the NCBI Sequence Read Archive (SRA; <http://www.ncbi.nlm.nih.gov/sra>) under accession number SRP044260. OutKnocker is available as open source software at <http://www.OutKnocker.org>.

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*Author contributions:* J.L.S.-B., T.S., and V.H. developed the methodology, designed the experiments, analyzed the data, and wrote the manuscript. J.L.S.-B. programmed the software and J.L.S.-B. and T.S. performed most of the experiments. T.S.E. established the THP-1 targeting. M.M.G. performed the TLR2 studies, whereas K.P. and E.L. performed the UNC93B1 experiments. V.H. conceived and supervised the study.

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