

Efficient combinatorial targeting of RNA transcripts in single cells with Cas13 RNA Perturb-seq

Received: 4 January 2021

Accepted: 24 October 2022

Published online: 22 December 2022

 Check for updates

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Pooled CRISPR screens coupled with single-cell RNA-sequencing have enabled systematic interrogation of gene function and regulatory networks. Here, we introduce Cas13 RNA Perturb-seq (CaRPool-seq), which leverages the RNA-targeting CRISPR–Cas13d system and enables efficient combinatorial perturbations alongside multimodal single-cell profiling. CaRPool-seq encodes multiple perturbations on a cleavable CRISPR array that is associated with a detectable barcode sequence, allowing for the simultaneous targeting of multiple genes. We compared CaRPool-seq to existing Cas9-based methods, highlighting its unique strength to efficiently profile combinatorially perturbed cells. Finally, we apply CaRPool-seq to perform multiplexed combinatorial perturbations of myeloid differentiation regulators in an acute myeloid leukemia (AML) model system and identify extensive interactions between different chromatin regulators that can enhance or suppress AML differentiation phenotypes.

Recent technological advances that couple pooled genetic perturbations with single-cell RNA-sequencing (scRNA-seq) or multimodal characterization (that is, Perturb-seq, CRISPR droplet sequencing, CRISP-seq and expanded CRISPR-compatible cellular indexing of transcriptomes and epitopes by sequencing (ECCITE-seq)^{1–4}), promise to transform our understanding of gene function. In particular, the ability to perform combinatorial perturbations represents an opportunity to decode complex regulatory networks, with pioneering work demonstrating the ability to identify epistasis and other genetic interactions^{5–7}. However, there are specific technical and analytical challenges associated with pooled single-cell screens that are exacerbated when considering combinatorial perturbations. For example, undetected or incorrectly assigned single-guide RNAs can affect up to 20% of cells⁶; this is compounded when multiple independent sgRNAs are introduced and independently detected in each cell. Moreover,

perturbations introduced by Cas9 are not uniformly efficient, and a considerable fraction of targeted cells may exhibit no phenotypic effects of perturbation^{8,9}. Therefore, when performing two or more simultaneous perturbations, the fraction of cells where all perturbations are both successfully introduced and successfully detected can decrease dramatically.

Type VI CRISPR–Cas proteins, such as the VI-D family member RfxCas13d, are programmable RNA-guided and RNA-targeting nucleases that enable targeted RNA knockdown. Notably, RfxCas13d is also capable of processing a CRISPR array into multiple mature CRISPR RNAs (crRNAs)¹⁰, presenting an attractive option for combinatorial perturbations at the RNA level. Recently, we confirmed that RfxCas13d can lead to striking target-RNA knockdown, and learned a set of optimal targeting rules from thousands of guide RNAs tiling multiple transcripts¹¹. We therefore sought to combine pooled CRISPR–Cas13

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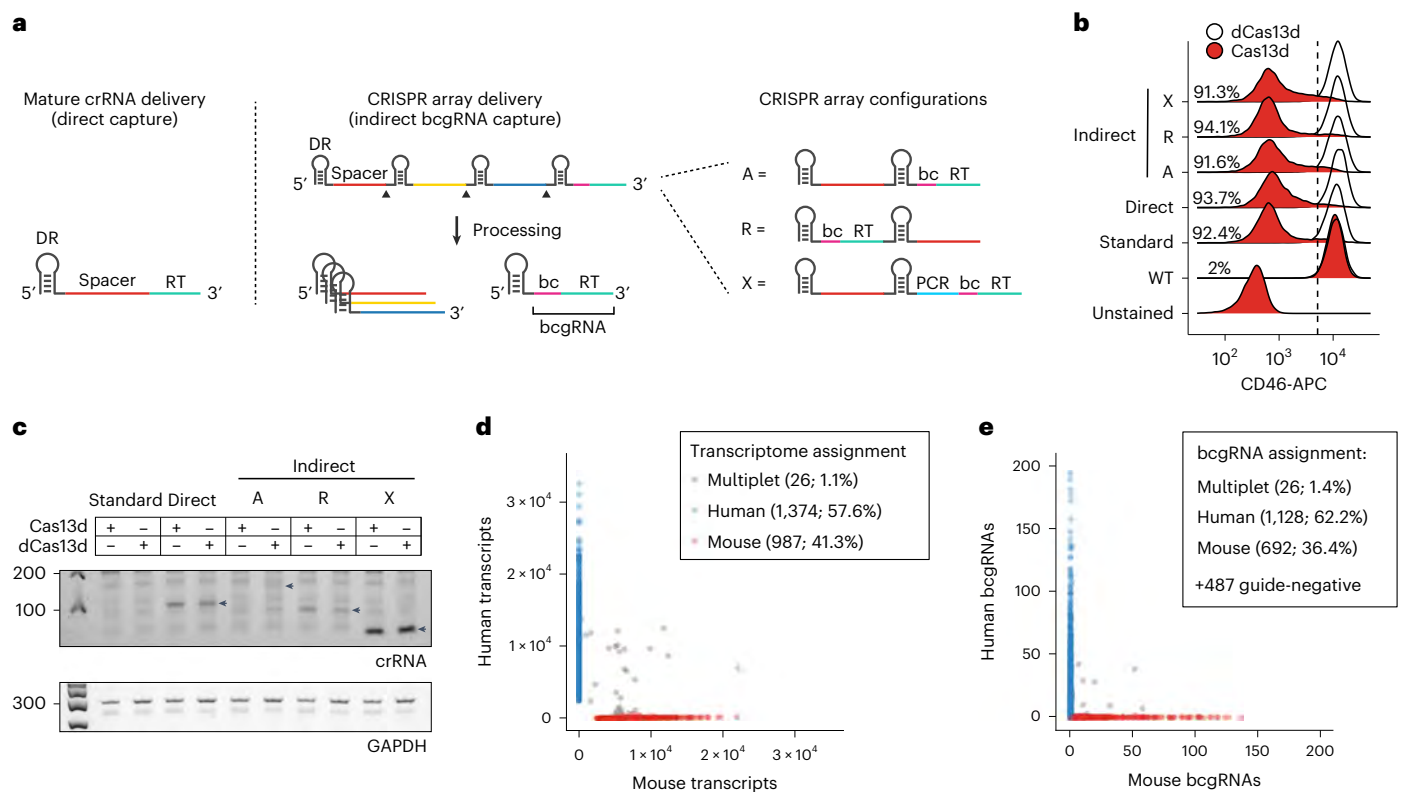


Fig. 1 | Efficient capture of gRNAs for CaRPool-seq. a, Scheme of direct and indirect array-based gRNA capture approaches. Direct capture uses a reverse transcription (RT) handle added directly downstream to the gRNA. For the indirect capture method, a bcgRNA is captured as a cleavable part of a CRISPR array. Three different CRISPR array configurations (A, R and X) have been tested (bc, barcode; PCR, PCR primer annealing site; A, array; R, reversed array configuration; X, extra PCR handle). **b**, Density plots showing the CD46-APC signal on Cas13d-mediated CD46 knockdown (red) and dCas13d-mediated controls (white) using the four CaRPool-seq configurations described in **a**, as well as standard gRNA. The CS1 reverse transcription handle was used in all cases. $N > 5,000$ cells examined per sample. **c**, PCR amplicons of reverse-

transcribed crRNAs from lentivirally infected cells used in **b** of one representative experiment. Expected product sizes: Direct capture 109 bp, A-type and R-type array 99 bp, X-type array 52 bp, unprocessed A-type array (159 bp). **d**, Species-mixing experiment profiling 2,387 HEK293FT-Cas13d or mouse NIH/3T3-Cas13d cells lentivirally transduced with CRISPR array virus. The CRISPR array includes a NT gRNA and a bcgRNA in X-type configuration. Axes show the number of transcripts associated with each cell barcode. Datapoint colors and boxed labels are assigned based on transcriptome classification (Methods). **e**, Number of bcgRNAs associated with each cell barcode. Datapoint colors are based on transcriptome classification, and boxed labels are based on observed bcgRNA.

screens with single-cell readouts to perform combinatorial and multimodal pooled genetic screens.

Results

Engineered CRISPR arrays enable Cas13 gRNA capture in single cells

Our method for Cas13 RNA Perturb-seq (CaRPool-seq) is enabled via an optimized molecular strategy to deliver individual or multiple gRNA perturbations in each cell and detect their identity during a single-cell sequencing experiment. Type VI-A, C and D Cas13 crRNAs consist of a short 5' direct repeat and a variable spacer (also called gRNA) at the 3' end, and therefore lack a common priming site for reverse transcription (RT). We developed two alternative approaches for Cas13 gRNA detection: (1) 'direct' capture, which adds a 'capture sequence' to the 3' end of the 23-nt target spacer (Fig. 1a); and (2) an 'indirect' capture strategy, where a dedicated crRNA of the CRISPR array contains an array specific barcode (barcode gRNA, bcgRNA) with different positional configurations of the bcgRNA within a CRISPR array (Fig. 1a). We evaluated the performance of each method by targeting cell surface proteins and measuring knockdown via flow cytometry (Fig. 1b and Extended Data Fig. 1), and by quantifying crRNA detection via PCR with reverse transcription (Fig. 1c). While all methods successfully induced robust knockdown (Fig. 1b), we found that indirect guide capture with an optimized configuration resulted in the strongest crRNA transcript

detection ability (configuration X, Fig. 1c), for both catalytically active and inactive Cas13 proteins.

These results demonstrate that RfxCas13d crRNAs can be modified by adding a common reverse transcription handle either directly to the gRNA or as a separate bcgRNA as part of a CRISPR array, allowing for reverse transcription and amplification. Notably, our strategy for indirect detection is well-suited for delivering multiple gRNAs into a single cell alongside a detectable bcgRNA that encodes the collective identity of these perturbations. In addition, using a unique set of reverse transcription handle and Illumina PCR priming sequence in our modified crRNA (Extended Data Fig. 2) ensures that these perturbations can be detected not only alongside scRNA-seq, but also when profiling additional molecular modalities (for example, CITE-seq¹² for simultaneous transcriptome and surface protein profiling).

As proof of principle, we first tested the ability of CaRPool-seq to detect and assign bcgRNAs in a single-cell species-mixing experiment. We separately transduced RfxCas13d-expressing human embryonic kidney 293FT (HEK293FT) and mouse NIH/3T3 cells with a viral pool of three CRISPR arrays containing a nontargeting (NT) gRNA and a species-specific bcgRNA. We profiled a mixture of human and mouse cells with the 10X Genomics Chromium system (v.3), aiming to detect both cellular transcriptomes and the bcgRNAs. Of 2,387 cells, we found that 78.5% expressed a single bcgRNA (1.1% >1 bcgRNAs; 20.4% no detected bcgRNA). Moreover, we observed extremely high

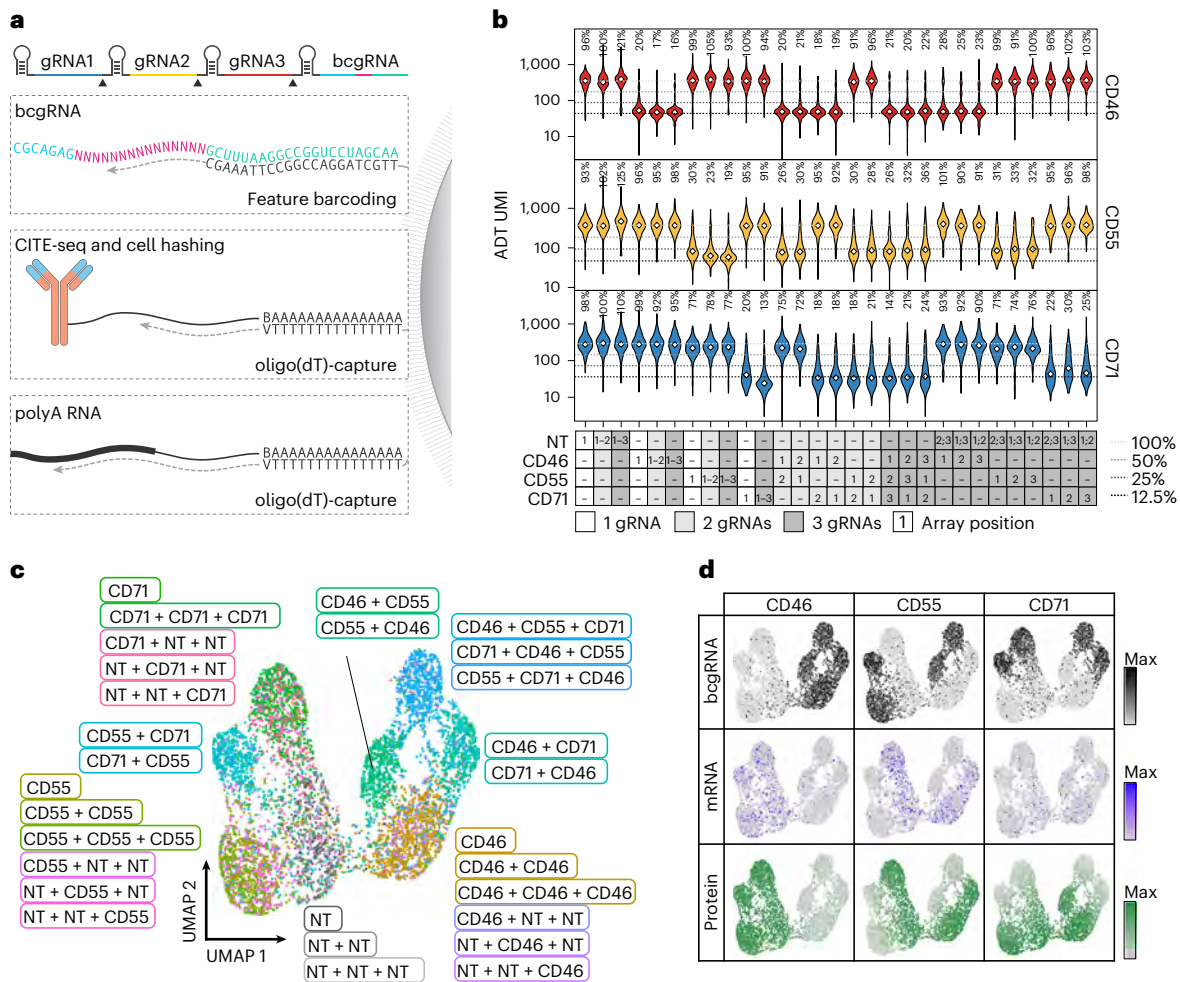


Fig. 2 | CaRPool-seq enables combinatorial gene targeting with a multimodal single-cell readout. **a**, CaRPool-seq can be combined with CITE-seq and Cell Hashing modalities. **b**, Violin plots depicting protein expression of target genes (ADT UMI counts for CD46, CD55, CD71), grouped by CRISPR arrays ($n = 29$; median number of cells 269; s.d. 97 cells). Three dashed lines indicate 50, 25 and 12.5% UMI count relative to the median of all NT cells. Diamonds indicate the median UMI count. The number above each violin plot indicates the mean

level of reduction across single cells. CD71 + CD71 was not included in the experiment. **c**, UMAP visualization of single-cell protein expression profiles of CaRPool-seq experiment ($n = 6,986$ cells). Cells are colored based on the single or combinatorial perturbations they received. **d**, Expression levels of bcgRNA (black), mRNA (blue) and protein (ADT, green) for CD46, CD55, CD71 superimposed on the UMAP visualization ($n = 6,986$ total cells).

concordance between RNA and bcgRNA labels in singlet cells (99.2%) (Fig. 1d,e). These numbers demonstrate that CaRPool-seq enables pooled perturbation screens that can be efficiently and accurately demultiplexed into a single-cell readout.

CaRPool-seq enables combinatorial gene targeting with multimodal single-cell readout

Next, we tested the ability of CaRPool-seq to distinguish combinatorial perturbations on multiple molecular modalities at single-cell resolution. We designed gRNAs targeting three cell surface proteins, CD46, CD55 and CD71, as well as NT gRNAs. We created 29 crRNA arrays (Supplementary Tables 1 and 2), each of which contains up to three gRNAs and a bcgRNA, allowing for the perturbation of these genes individually or in combination. We transduced HEK293FT cells with a viral pool of all crRNAs and performed CaRPool-seq with CITE-seq¹² readout (Fig. 2a and Extended Data Fig. 3a), allowing the assessment of each perturbation on both the cellular transcriptome and antibody-derived tags (ADTs) associated with CD46, CD55 and CD71 surface protein levels.

We obtained 9,355 single-cell profiles and demultiplexed them into groups based on the detected bcgRNA (Extended Data Fig. 3b; 74.7% expressed a single bcgRNA, 80.8% expressed at least one bcgRNA). We

observed, on average, a 76.5% ($\pm 5.7\%$) mean reduction in protein levels for each targeted gene after perturbation with Cas13 demonstrating clear evidence of robust molecular perturbation (Fig. 2b–d). Moreover, the strength of knockdown was similar for multi-gRNA crRNA arrays relative to single gRNA perturbations (Fig. 2b and Extended Data Fig. 3c–e). When examining transcriptomic pseudobulk profiles for all 26 targeting gRNA groups, we observed decreased messenger RNA expression for each targeted transcript, even when perturbing transcripts of three genes simultaneously (15 examples in Extended Data Fig. 3f,g). The average strength of transcriptomic knockdown (mean 65%, s.d. 8.7%) was consistently reduced compared to the observed protein reduction. Target RNAs are continuously being produced and degraded before the target can be translated into protein. Further, analogous to how Cas9-nuclease targeting often produces RNAs degraded by nonsense mediated decay¹³, it is possible that Cas13 cleavage produces RNA molecules that can be detected by scRNA-seq but cannot be translated into functional protein¹⁴, suggesting that the level of measured RNA knockdown underestimates the phenotypic effect of Cas13 perturbation.

We performed several analyses to demonstrate that Cas13d-mediated gene knockdown does not introduce notable off-target effects or deleteriously alter cellular fitness. We identified

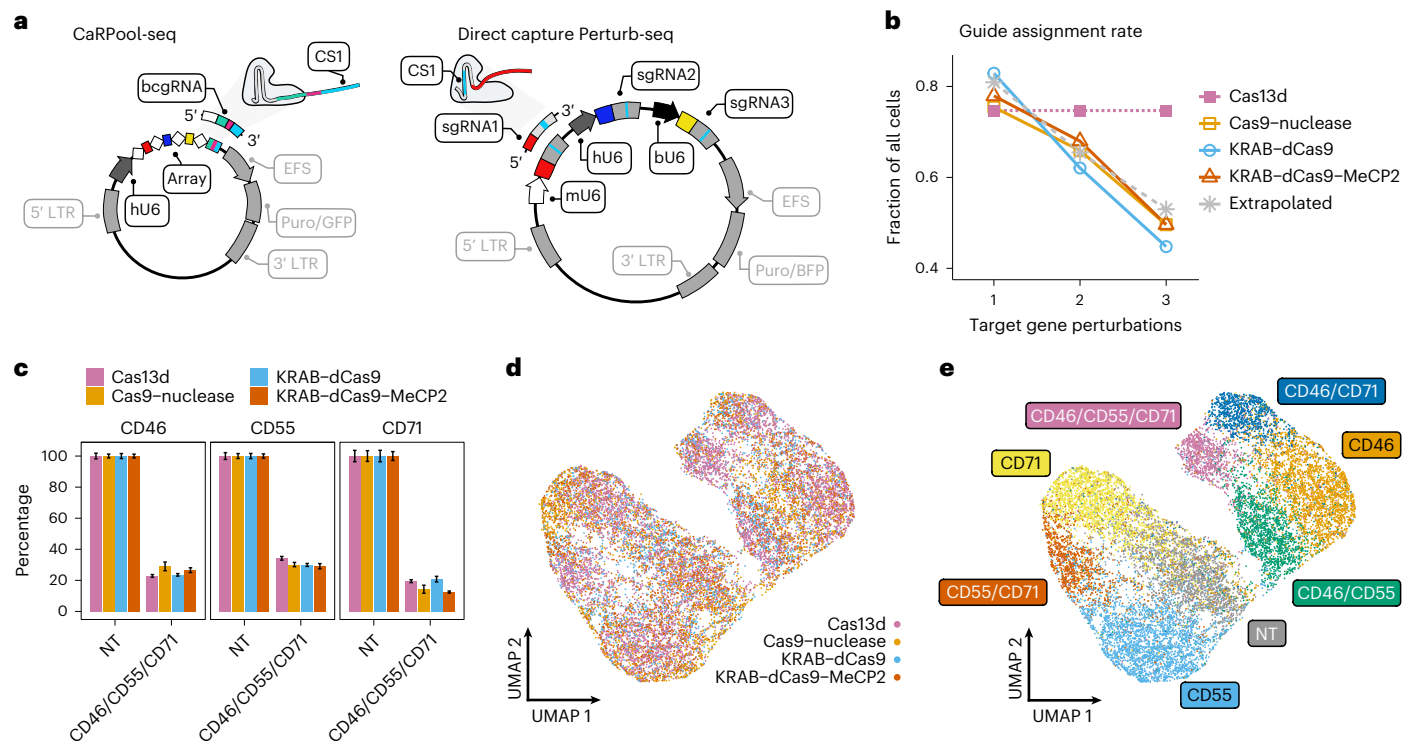


Fig. 3 | Benchmarking CaRPool-seq against alternative combinatorial perturbation approaches. **a**, Plasmid vectors for lentivirus production for triple perturbation scenarios comparing CaRPool-seq and Direct Capture Perturb-seq⁶. **b**, Fraction of cells where the correct combination of gRNA was detected for single, double and triple perturbations. The dashed gray line represents a theoretical extrapolation based on an assumption of independent sgRNA detection with $P = 0.81$ (ref.⁶). **c**, Relative expression of cell surface proteins CD46, CD55 and CD71 in cells with assigned NT (s)gRNAs or a combination of three

targeting (s)gRNAs (NT, $n = 448, 711, 510, 577$; CD46/CD55/CD71, $n = 874, 55, 142, 89$ for Cas13d, Cas9-nuclease, KRAB-dCas9 and KRAB-dCas9-MeCP2, respectively). The expression level of each target is normalized to NT control. Bars indicate mean across cells with s.e.m. error bars. **d**, Protein level ADT-based clustering of single-cell expression profiles of merged CaRPool-seq ($n = 6,986$), Perturb-seq experiments using Cas9 ($n = 2,836$), KRAB-dCas9 ($n = 2,911$) or KRAB-dCas9-MeCP2 ($n = 3,038$). Cells are colored by perturbation technology. **e**, As for **d**. Cells are colored based on the single or combinatorial perturbation received.

eight genes whose sequence contains potential off-target binding sites for any of our three perturbations, but found that the expression of these genes was not significantly changed in our CaRPool-seq data (Extended Data Fig. 4a). We also performed CD55 target knockdown followed by more sensitive bulk RNA-seq and found no evidence for elevated levels of Cas13d off-targets (Extended Data Fig. 4b and Supplementary Table 3). In addition, previous reports have suggested that expression and target-dependent activation of Cas13d can induce broad nonspecific degradation of cytoplasmic and nuclear mRNA, and a reduction in cellular proliferation or fitness¹⁵. Notably, transcripts of mitochondrial genes have been suggested to be at least partially protected from Cas13d collateral activity¹⁵. Hence in the presence of collateral activity, mitochondrial genes may appear relatively upregulated compared to nuclear and cytoplasmic genes. Therefore, we compared mitochondrial gene expression levels in cells that have received one or more targeting gRNAs compared to NT control cells (Extended Data Fig. 4c), and did not observe upregulation in our CaRPool-seq data. Last, we classified cell cycles stage for each cell, and found no difference in cell cycle distributions (indicative of their proliferation state) compared to NT control cells (Extended Data Fig. 4d-f). Our findings likely reflect CaRPool-seq's controlled delivery of Cas13d and gRNAs using single integration lentiviral systems instead of transient overexpression, which is consistent with the suggestion that lower and more controlled Cas13 expression can mitigate collateral activity¹⁶.

CaRPool-seq efficiently recovers cells with multiple perturbations

We next benchmarked the performance of CaRPool-seq against direct capture Perturb-seq⁶ using three different Cas9 effectors:

Cas9-nuclease, a first-generation CRISPR inhibition (CRISPRi) system, Krüppel associated box (KRAB) fused to dCas9 (refs.^{17,18}) and a second-generation, dual-effector CRISPRi system, KRAB-dCas9-MeCP2 (refs.^{18,19}). In CaRPool-seq one bcgRNA encodes the combined gRNA identities, while direct capture Perturb-seq requires independent detection of one sgRNA feature per perturbation (Fig. 3a). We replicated our previously described experimental system, targeting the same three cell surface markers (CD46, CD55 and CD71) alone or in combination. For each target, we evaluated three sgRNAs from established CRISPR-KO²⁰ and CRISPRi²¹ sgRNA libraries (Extended Data Fig. 5a) and selected the best sgRNA for Perturb-seq (Extended Data Fig. 5b). In addition, we used Cell Hashing²² to label cells targeted with vectors encoding single, double or triple perturbations. As in CaRPool-seq, we quantified gRNA, RNA and ADT levels in each cell.

Our benchmarking analysis found that, in contrast to CaRPool-seq, alternative Cas9-based approaches struggled to efficiently identify and detect combinatorial perturbations (Fig. 3b). For example, in the KRAB-dCas9-MeCP2 experiment, we recovered 1,570 cells that received vectors targeting three genes. Among these cells, only 779 (49.6%) were associated with the correct three sgRNA after sequencing. In the remaining cells, we detected too few perturbations (zero, one or two gRNAs, 31.2%), too many (four or more gRNAs 10.0%), or an improper combination of three gRNA (9.2%). This observed drop-off is fully consistent with the theoretical expectation of recovery for multiple independently detected gRNAs and highlights the challenge of efficiently profiling multiple perturbations with existing approaches. Since CaRPool-seq associates combinatorial perturbations with a single bcgRNA, the efficiency of detection does not vary between single and multiple perturbations.

We next compared the strength of perturbation across methods. We first considered cells where three perturbations were successfully detected based on either the bcgRNA (CaRPool-seq) or independently detected gRNA (Perturb-seq). When considering these cells, all methods successfully induced a similarly strong depletion of all three surface proteins (Cas13d 74.5%, Cas9 75.5%, KRAB-dCas9 75.2%, KRAB-dCas9-MeCP2 77.3%) (Fig. 3c and Extended Data Fig. 5c,d). We next analyzed all cells based on their ADT levels. CaRPool-seq and Perturb-seq cells clustered together (Fig. 3d), and grouped by gRNA identity (Fig. 3e and Extended Data Fig. 5e), again demonstrating that the strength of phenotypic protein perturbation was similar across all methods. We conclude that CaRPool-seq and Perturb-seq can both effectively introduce combinatorial perturbations into single cells. However, CaRPool-seq exhibits clear advantages in the ability to successfully identify and detect these perturbations and therefore represents an attractive approach for performing combinatorial single-cell CRISPR screens.

A pooled RNA-targeting CRISPR screen identifies genes involved in acute myeloid leukemia (AML) differentiation

To demonstrate the throughput and potential of CaRPool-seq to characterize genetic interactions, we performed a multiplexed screen of 158 combinatorial gene pairs. Motivated by recent work²³, we aimed to characterize potential interactions between previously identified regulators of leukemic differentiation, which can influence the response to chemotherapy and small-molecule drugs. We generated a human MLL-AF9 NRAS^{G12D} AML cell line (THP1 cells), with a stably integrated doxycycline-inducible Cas13d cassette, as a model system. We first performed a bulk Cas13d CRISPR screen using a targeted library of 439 genes with ten gRNA per gene. On day 13–16 post-Cas13d induction, cells were sorted into bins based on their surface expression of CD14 and CD11b, immunophenotypic markers of monocyte differentiation. By comparing gRNA representation between low and high-expressing bins, we selected 26 genes that influenced differentiation consistently across multiple independent gRNAs and that have also been identified previously in orthogonal pooled Cas9 screens²³ (Extended Data Fig. 6a–h and Supplementary Table 4). Through individual perturbations with a flow-cytometry readout, we found that target gene perturbations led to detectable CD11b expression changes after 3 days (Extended Data Fig. 6i). Consistent with previous work²³, these genes were largely associated with DNA-binding and chromatin remodeling functions, and include a subset of previously identified regulators of AML differentiation.

CaRPool-seq identifies genetic interactions in AML differentiation

We next applied CaRPool-seq to test the effects of combinatorially perturbing these regulators (Fig. 4a and Extended Data Fig. 7a). We infected cells with a pooled library of 385 crRNA arrays. This library encoded 28

single perturbations (26 regulators and two negative control genes) and 158 paired perturbations. It also encompassed technical replicates for each perturbation using two independent gRNAs, as well as NT controls. We profiled the transcriptome, cell surface protein levels and gRNA expression for 31,308 demultiplexed single cells.

We first compared the level of surface protein expression for each perturbation to NT controls (Extended Data Fig. 7b). As expected, we found that each single-gene perturbation affected CD11b expression, with observed \log_2 fold changes that were in strong agreement with the level of gRNA enrichment from bulk CRISPR screens ($R = 0.86$; Fig. 4b, Extended Data Fig. 7c–e and Supplementary Table 5). Observed \log_2 fold changes for all perturbations were also reproducible ($R = 0.82$, Extended Data Fig. 7f) across technical replicate perturbations when comparing effects measured for independent gRNAs. We next compared the observed effects of the 158 dual gene perturbations to the effects resulting from the two corresponding single perturbations. We observed a strong correlation and found that the dual perturbation was typically stronger than the average of individual knockdowns, but weaker than the product (Fig. 4c). We also observed both synergistic and dampening effects. For example, individual knockdown of the histone demethylase KDM1A (\log_2 FC 2.41) and the histone deacetylase HDAC3 (\log_2 FC 0.53) lead to strong and weak CD11b upregulation, respectively, but dual perturbation led to a synergistic effect (\log_2 FC 2.85). In contrast, while individual knockdown of EP300 also leads to CD11b upregulation (\log_2 FC 1.57), dual perturbation with KDM1A (\log_2 FC 2.05) was weaker than the individual KDM1A knockdown. We observed similar findings using data from our Cas13d CD11b pooled screen (Extended Data Fig. 7g and Supplementary Table 5). To further validate the synergistic relationship between KDM1A and HDAC3 we infected KRAB-dCas9-MeCP2 expressing THP1 cells with multiple independent sgRNAs and measured CD11b and CD14 cell surface protein expression 7 days postinfection using flow cytometry. Again, we observed synergistic upregulation of both surface markers (Fig. 4d) after dual perturbation.

We next explored the transcriptional profiles in our CaRPool-seq dataset. We first sought to orthogonally validate the transcriptomic signatures we observed on perturbation of single genes by comparing with alternative technologies and datasets. We found that the differential gene expression signatures for single-gene perturbations obtained using ECCITE-seq (5' scRNA-seq, Cas9 perturbation)²³ can be readily reproduced in our CaRPool-seq (3' scRNA-seq, Cas13d perturbation) data (Extended Data Fig. 8a,b). These differentially regulated gene modules were typically associated with genetic programs associated with the differentiation and function of myeloid cells (Extended Data Fig. 8c). To further explore comparisons between human hematopoiesis and our in vitro model system, we integrated our CaRPool-seq dataset with an scRNA-seq reference of hematopoietic progenitors and mature myeloid cells from the Human Cell Atlas and Human Biomolecular Atlas

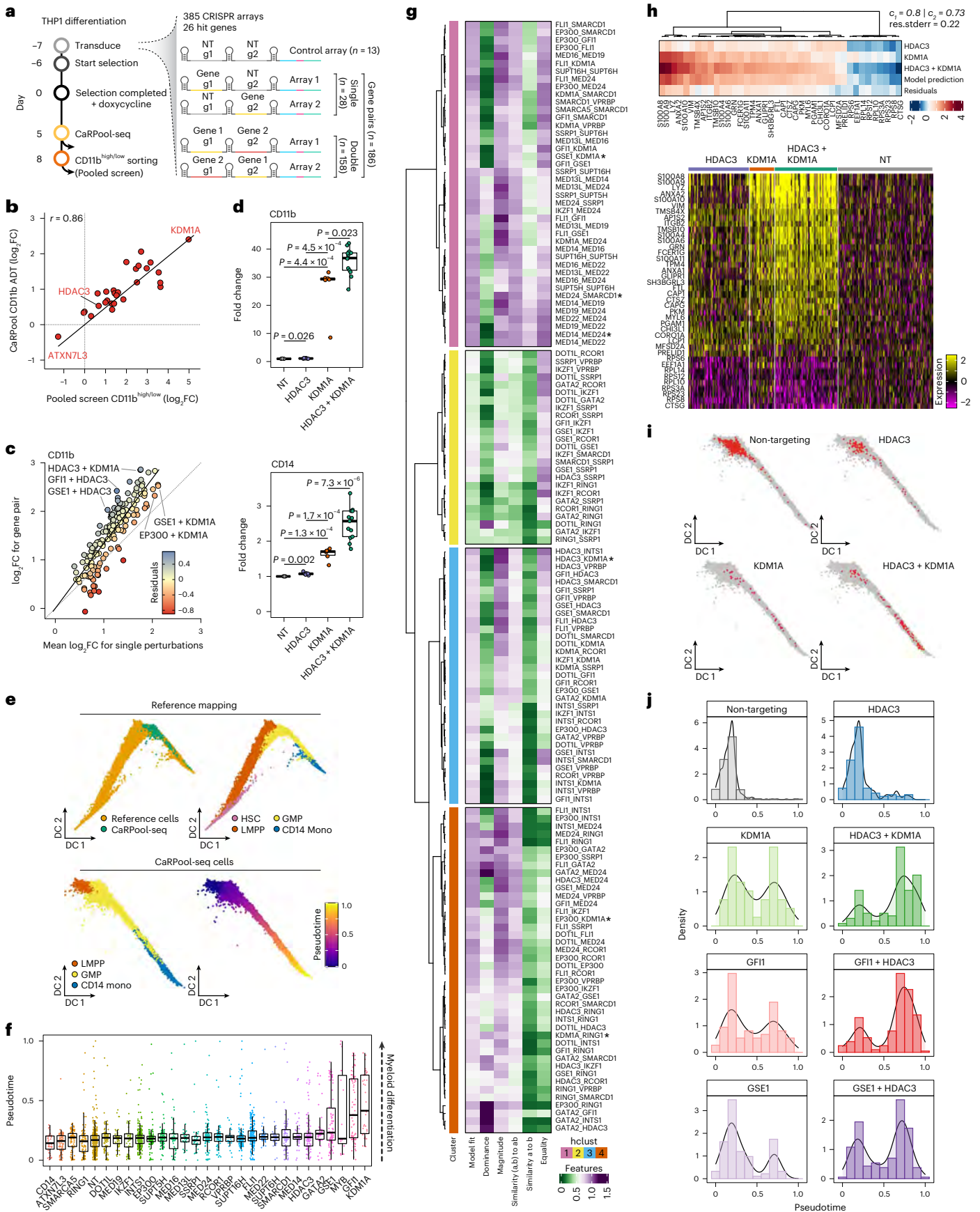
Fig. 4 | CaRPool-seq identified genetic interactions in AML differentiation.

a, Timeline for THP1 cell infection, CaRPool-seq and pooled screen for CD11b expression. Pooled lentivirus library encodes 385 CRISPR arrays, with 158 gene pair perturbations, 28 single-gene perturbations (each with two nonoverlapping gRNAs (technical replicate); single, gene_g1/NT_g2 and NT_g1/gene_g2; pair, geneA_g1/geneB_g2 and geneA_g2/geneB_g1) and 13 NT controls. **b**, Correlation of bcgRNA enrichment in the pooled screen (CD11b^{high/low}) and CD11b ADT \log_2 FC for cells grouped by bcgRNA cells relative to control cells in CaRPool-seq. **c**, Correlation of CD11b ADT \log_2 FC of cells with dual perturbations, and the mean \log_2 FC of both single perturbations ($n = 158$ gene pairs). Residuals indicate the distance to the average linear relationship. **d**, Relative cell surface marker expression. Monoclonal THP1 KRAB-dCas9-MeCP2 cells were infected with dual sgRNA lentiviral particles, carrying 0, 1 or 2 targeting sgRNAs (NT + NT $n = 3$; KDM1A + NT $n = 6$; HDAC3 + NT $n = 6$; KDM1A + HDAC3 $n = 13$ combinations). Puromycin-selected cells were stained for CD11b (top, PE-Cy7) and CD14 (bottom, APC) 7 days posttransduction. Shown is the mean fluorescence intensity (>5,000 cells per sample) for each sample compared to the mean

fluorescence intensity of the three NT samples (one-tailed *t*-tests). **e**, Diffusion map showing THP1 CaRPool-seq cells integrated into a subset of a human bone marrow reference (see Methods). Pseudotemporal ordering was performed jointly on all cells and is shown for CaRPool-seq ($n = 30,707$) separately. **f**, Pseudotime quantification of singly perturbed cells (total cells, $n = 2,612$; single-gene perturbation, median $n = 74$ cells; s.d. $n = 86$ cells). **g**, Regression model results decomposing the observed dual perturbation responses as a linear combination of single-gene perturbation responses (Methods). **h**, Comparison of transcriptional responses for dual versus single perturbation. Heatmap shows deviation in average gene expression relative to unperturbed cells for the 20 most significantly regulated genes (Wilcoxon's rank-sum test). Average heatmap (top) is accompanied by single-cell gene expression heatmap (bottom) (HDAC3 $n = 96$ cells, KDM1A $n = 36$ cells and HDAC3 + KDM1A $n = 99$ cells). **i**, CaRPool-seq diffusion map as in **e** highlighting cells that have received indicated gRNAs. **j**, Quantification of pseudotemporal ordering of perturbed cells. Boxes in **d** and **f** indicate the median and interquartile ranges, with whiskers indicating 1.5 times the interquartile range.

Project^{24–27}, aligning CaRPool-seq THP1 cells to their closest neighbors in the reference dataset, and constructing a joint differentiation trajectory (Fig. 4e). We found that NT control cells localized to early points,

but that single perturbations (that is, KDM1A, GF11, GSE1) pushed cells further down the differentiation trajectory (Fig. 4f), consistent with their role in enhancing leukemic differentiation.



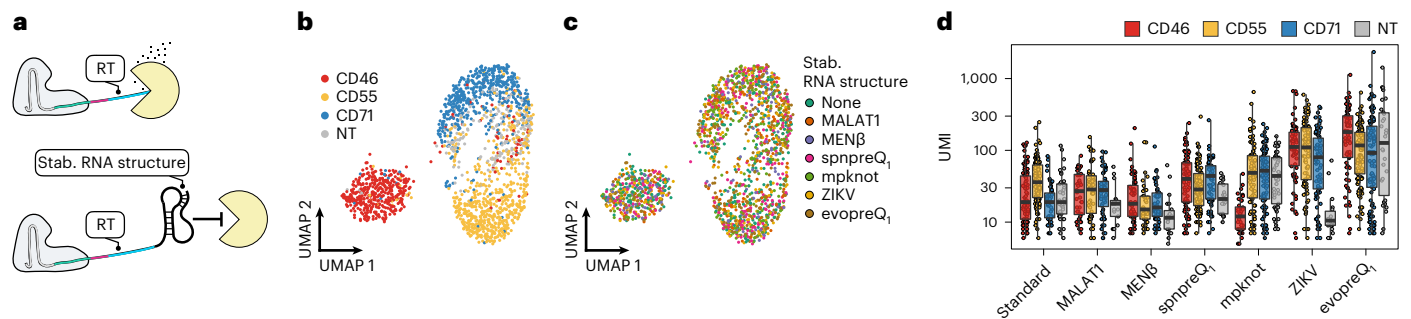


Fig. 5 | Stable RNA structures improve bcgRNA detection in CaRPool-seq experiments. **a**, Model of 3' exonucleolytic decay of bcgRNAs when embedded in CRISPR-Cas13d ribonucleoprotein complex. RT represents the reverse transcription handle. **b**, UMAP visualization of single-cell protein expression profiles of CaRPool-seq experiment ($n = 1,770$ cells). The experiment included four different gRNAs (NT control, CD46, CD55 and CD71) in combination with one out of seven different stabilizing elements. Cells are colored based on the single perturbations they received. **c**, UMAP visualization of single-cell protein

expression profiles of CaRPool-seq experiment as shown in **b**. Cells are colored based on the structured RNA element they received (no stabilizing element (standard) or one of the six shown in Extended Data Fig. 9a). **d**, UMI counts for the assigned bcgRNA for each cell separated by target gene and RNA stabilizing element. UMI counts $>2,000$ are not shown. Boxes indicate the median and interquartile ranges, with whiskers indicating 1.5 times the interquartile range (total cells $n = 1,770$; conditions $n = 28$; cell per condition, median $n = 63$ cells; s.d. $n = 30$ cells). ZIKV, zika virus.

We applied a recent pioneering framework⁷ that fits a regression model to decompose the observed perturbation responses in doubly perturbed cells as a linear combination of single-gene perturbation responses. The fit and coefficients of this model describe multiple types of genetic interaction, including epistasis, genetic suppression and synergistic relationships. Fitting these models to each of our pairwise perturbations revealed a diversity of genetic interactions, which we broadly clustered into four groups (Fig. 4g). For 33 gene pairs in cluster 1, we saw that each individual gene's profile contributed equally to the dual perturbation response and the linear model exhibited a strong fit. As a positive control, many of the pairs in this cluster represented perturbations of two proteins in the same complex (that is, MED14/MED24, SUPT16H/SUPT6H), which show similar gene expression responses for singly and doubly perturbed cells (Extended Data Fig. 8d–f). This cluster also represented pairs of proteins residing in separate complexes (MED24/SMARCD1 of mediator and SWI/SNF complexes), which share similar perturbation signatures (Extended Data Fig. 8d). Dual perturbation of KDM1A and the transcriptional repressor GSE1 also fell in this cluster (Extended Data Fig. 8f), consistent with previous work that suggests a cooperative interaction via colocalization at repressed promoters to inhibit myeloid differentiation²⁸.

In cluster 4, we identified genetic interactions where one gene's effect appeared to dominate over the other. We generally observed that transcriptional responses varied widely when pairing KDM1A knockdown with different chromatin regulators. For example, we found that the EP300-signature appeared more strongly than the KDM1A-signature when combinatorial perturbing both genes (Extended Data Fig. 8g). Dually perturbed cells exhibited higher expression of progenitor genes (that is the progenitor marker AZU1), and reduced expression of differentiated marker genes (that is, myeloid marker S100A4) compared to individual KDM1A perturbation. In contrast, the KDM1A response signature dominated when paired with perturbation of the polycomb repressive complex member RING1 (Extended Data Fig. 8h). Dual perturbation of HDAC3 enhanced the KDM1A transcriptional response signature (Fig. 4h), consistent with our previously described immunophenotypic results for these cells (Fig. 4c). This transcriptional response led dually perturbed cells to be distributed at later segments of our integrated myeloid differentiation trajectory, exhibiting enhanced differentiation compared to either single perturbation (Fig. 4i,j). These findings support and provide a molecular explanation for recent observations that combination therapies of KDM1A antagonist and HDAC inhibitors exhibit an enhanced response²⁹. Moreover, we identified additional synergistic

combinations between HDAC3/GFI and HDAC3/GSE1, both of which enhanced the expression of immunophenotypic markers (Fig. 4c), as well as transcriptional differentiation state (Fig. 4j).

Stable RNA structures improve bcgRNA detection

While our paper was in review, Nelson et al.³⁰ reported that the inclusion of structured RNA motifs on prime editing gRNAs (pegRNAs) led to protection from exonuclease degradation, increased stability, and enhanced efficiency. While we expect that crRNA are typically protected from degradation while complexed with Cas13 (refs. 31,32), the ends of longer bcgRNA molecules may still be accessible and susceptible to degradation. These ends include reverse transcription priming sites that are essential for CaRPool-seq bcgRNA detection. Therefore, we tested the addition of stably structured stabilizing RNA elements at the 3' end of the bcgRNA to antagonize nucleolytic decay (Fig. 5a). We tested six different structures (Extended Data Fig. 9a), and repeated our benchmarking experiment targeting CD46, CD55 and CD71 in HEK293FT cells. While protein knockdown was indistinguishable for all six structures (Fig. 5b,c and Extended Data Fig. 9b), we found that two elements (Zika virus-derived xrRNA1 dumbbell³³; evopreQ₁ pseudoknot³⁴) led to a robust increase in bcgRNA unique molecular identifier (UMI) counts (Fig. 5d). In particular, the evopreQ₁ pseudoknot element led to a sixfold higher bcgRNA detection UMI counts compared to our initial design (Extended Data Fig. 9c). The increased sensitivity also systematically improved the signal-to-noise ratio to distinguish true bcgRNA UMI counts from spurious secondary bcgRNA UMI counts (Extended Data Fig. 9d). This modified bcgRNA structure therefore further improves the performance of CaRPool-seq, and is recommended for future experiments.

Discussion

Here, we present CaRPool-seq, a flexible method for performing CRISPR-Cas13 RNA-targeting screens with a single-cell sequencing-based readout. We introduced an optimized strategy to deliver multiple gRNA as part of a single CRISPR array, which is subsequently cleaved into individual crRNAs. We demonstrate that this strategy is well-suited for performing combinatorial perturbations, whose identity is encoded in a single barcode that can be reliably detected alongside multiple molecule modalities including scRNA-seq and CITE-seq.

Through benchmarking, we show that CaRPool-seq is more efficient and accurate when assigning multiple perturbations in single cells when compared to Cas9-based technologies. Even with

individual perturbations, the user can still benefit from CaRPool-seq. In particular, as an RNA-targeting enzyme, Cas13d can be uniquely applied to target specific RNA isoforms, or even circular, enhancer or antisense RNA molecules. RNA-directed approaches may also be optimal when targeting a single member of a local gene cluster, where alternative KRAB-mediated repressive strategies may ‘spread’ and introduce off-target effects³⁵. CaRPool-seq can profile additional cellular modalities such as cell surface protein levels and, in the future, can be extended to additional molecular modalities including intracellular protein levels and chromatin accessibility. Moreover, the strategy of introducing multiple perturbations through cleavable arrays is extendable to other CRISPR systems, including Cas12 (ref.³⁶) and Cas7-11 (ref.³⁷), and represent promising extensions of this work. And as combinatorial screens scale rapidly, we note that CaRPool-seq is compatible with pioneering approaches for targeted scRNA-seq, including hybridization-based 10X Targeted Gene Expression Panels⁶ or multiplexing PCR-based approaches³⁸.

There are current limitations with CaRPool-seq that may be overcome by future advances. For example, RNA-targeting CRISPR proteins cannot currently activate gene expression through transcription or translation in mammalian cells³⁹. Additionally, our work suggests a pooled cloning strategy for medium-sized CaRPool-seq CRISPR arrays; however, further optimizations may be required for long arrays with very large numbers of targeting gRNAs. Lastly, while we did not observe direct or indirect evidence for RfxCas13d’s promiscuous collateral activity in our CaRPool-seq experiments, other RNA-targeting CRISPR effectors^{37,40,41} may represent an alternative for future experiments.

Combinatorial screens have the potential to shed substantial new light on the structure of genetic regulatory networks, and also to identify combinatorial perturbations that achieve desirable cellular phenotypes. Our CaRPool-seq analysis of AML differentiation regulators benefited from recently developed computational frameworks to identify genetic interactions from multiplexed perturbation screens, and these types of data will be valuable resources for systematic reconstruction of complex pathways and cell circuits. Moreover, our identification of combinatorial perturbations that enhanced AML differentiation phenotypes was consistent with previous identification of efficacious multi-drug therapies, suggesting that future experiments may help to nominate candidates for combined drug treatments. We conclude that CaRPool-seq represents a powerful addition to the growing toolbox of methods for multiplexed single-cell perturbations.

Online content

Any methods, additional references, Nature Portfolio reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41592-022-01705-x>.

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Methods

Pooled Cas13d library design and cloning

We design two libraries for pooled cloning, one to identify genes that lead to THP1 cell differentiation (Extended Data Fig. 6) and one for combinatorial targeting with CaRPool-seq (Fig. 4).

First, we designed a RfxCas13d gRNAs library for single gRNA expression targeting 439 individual genes. We selected 240 genes that led to CD11b or CD14 upregulation in Cas9 screens²³, in addition to 199 control genes in TLR4-signaling. We selected the transcript with the highest isoform expression (CCLE, <https://sites.broadinstitute.org/ccle/datasets>) per gene and designed gRNAs using our Cas13d design algorithm¹¹. For each gene, we selected ten gRNAs from efficacy quartile Q4 (or Q3), spread along the coding region. Selected gRNAs had no secondary target sites with 0–2 mismatches to the cognate site⁴². In total, we designed 4,390 gRNAs and 410 NT control gRNAs (>3 mismatches to hg19-annotated transcripts). Library cloning has been described before¹¹. In brief, pooled oligonucleotides (Twist) were amplified using 8× PCR reactions with eight amplification cycles using direct repeat-specific forward primer (Supplementary Table 2). The amplicon was Gibson-cloned into pLentiRNAGuide_001 and pLentiRNAGuide_002 (Addgene nos. 138150 and 138151). Complete library representation with minimal bias (90th percentile/10th percentile crRNA read ratio of 1.8 for both libraries) was verified by Illumina sequencing (MiSeq).

For the CaRPool-seq library, we manually inspected all gRNA enrichments from the pooled screen library described above. For each target genes, we picked the two most enriched (depleted for CD14/ATXN7L3) gRNAs avoiding overlapping gRNAs. For each gene, we paired the two gRNAs with an NT gRNA ($n = 28$ single perturbations, $n = 56$ arrays). For 17 genes, we designed all pairwise combinations ($n = 136$ gene pairs, $n = 272$ arrays). For nine genes we designed a subset of possible gene pairs within the same complex ($n = 22$ gene pairs, $n = 44$ arrays). We added 13 NT control arrays. In total, we design 385 arrays with 186 single or double perturbations, each represented by two independent technical replicate gRNA combinations. For the bcgRNAs, we designed random 15mer sequences with hamming distance greater than four to one another. We balanced the relative CRISPR array abundance by the negative effect on cell proliferation of the targeted genes and increased the number of array copies in the pool to minimize dropout in the CaRPool-seq experiment. The oligos for synthesis were designed in the following way:

PCR-handle::BsmBI-site::gRNA1::DR::gRNA2::LguI-bridge::b
barcode::BsmBI-site::PCR-handle

Pooled oligonucleotides (Twist, Supplementary Tables 1 and 2) were amplified using Pfu-Ultra-II following the manufacturer's recommendation using 1 μ l of enzyme and 20 ng (1 ng μ l⁻¹) of the oligo pool in a 50 μ l reaction 95 °C/2 min, 5× (95 °C for 20 s, 58 °C for 20 s, 72 °C for 15 s), 72 °C for 3 min). The amplicon was 2× solid phase reversible immobilization (SPRI) purified, followed by BsmBI-digestion and additional 2× SPRI cleanup. All of the product was ligated into BsmBI-digested pLentiRNAGuide_003 (without evopreQ₁ sequence element) using T7-DNA ligase and cloned as described in ref.¹¹ with >1,000 colonies per construct. The resulting plasmid pool was digested with LguI to enable ligation of the third direct repeat and small RNA-handle to complete the bcgRNA and CRISPR array. The LguI insert (Supplementary Table 2) was cloned into pLentiRNAGuide_001, digested with LguI and gel-purified (2% eGel). Complete library representation with minimal bias (90th percentile/10th percentile crRNA read ratio 2.6/4.8), and correct gene pair to bcgRNA linkage (>94%) was verified by Illumina sequencing (MiSeq). During library cloning, we noticed two critical details: alternative polymerase KAPA and Q5 can lead to a stronger bias in relative array abundance. Further, reducing the number of PCR cycles with increased oligo pool input amounts can decrease bcgRNA reassortment. Last, while we chose a two-step cloning strategy, a single-step strategy may yield similar results. pLentiRNAGuide_003 has been deposited to Addgene (no. 192505).

Pooled CRISPR screening

Pooled Cas13d screens have been performed as described before in ref.¹¹, with minor modifications. Cas13d expression was induced after THP1 cells were fully selected (1 μ g ml⁻¹ doxycycline). Growth medium with fresh puromycin, blasticidin and doxycycline was replenished every 2–4 days, and cells were split as needed always maintaining a guide representation of >1,000×.

For the single gRNA pooled screen, we collected a 1,000× representation at 7 and roughly 14 days post-Cas13d induction and before sorting. After 2 weeks (13–16 days) we stained 15 million cells (roughly 3,000× representation), using FcX-blocking buffer (BioLegend no. 422302; 10 min at room temperature) and followed by either CD11b (BioLegend clone ICRF44 no. 301322, 4 μ l per 1 × 10⁶ cells per 100 μ l) or CD14 (BioLegend clone HCD14 no. 325608, 4 μ l per 1 × 10⁶ cells per 100 μ l) staining (30 min at 4 °C), and finally resuspending cells on PBS with DAPI (4,6-diamidino-2-phenylindole) (Sigma no. D9542, 0.4 μ g ml⁻¹) to detect any apoptotic or dead cells. We sorted the cells (Sony SH800) based on their signal intensities (CD11b or CD14: lowest 10–15% and highest 10–15%). Cells were PBS-washed and frozen at –80 °C until sequencing library preparation. In total, we prepared four independent transductions (two multiplicities of infection (MOI) and two alternative direct repeats), performed CD14 sorts for all four transduction replicates, and CD11b sorts for three transduction replicates collecting 1 × 10⁶ to 1.5 × 10⁶ cells per bin.

For the combinatorial perturbation pooled screen, we performed three transduction replicates (MOI 0.13–0.20). Eight days post-Cas13d induction, we collected an input representation (>1,000× coverage) and stained 20–30 million cells with FcX-blocking, CD11b and DAPI as described above. Cells were CD11b-sorted (lowest 15% and highest 15% signal intensity). Cells were PBS-washed and frozen at –80 °C until sequencing library preparation. Library preparations for the single gRNA pooled screen were done as described before¹¹. For the combinatorial targeting pooled screen, we adopted a PCR strategy similar to the CaRPool-seq bcgRNA readout. Pooled screen readout PCR1 remained unchanged. In PCR2, we amplified the 15 basepair (bp) barcode sequence using a soluble Nextera-Read1-CS1 feature capture primer including an optional 28 randomized bases mirroring UMI and cell barcode, and RPIx Read2 i7 index primer. The amplicon was completed in PCR3 using Feature SI primer 2 (10X Genomics) and P7 primer.

Pooled CRISPR screen analysis

Raw reads were demultiplexed based on Illumina i7 barcodes using bcl2fastq and, if applicable, by their custom in-read barcode using a custom python script. For the single gRNA pooled screen, read1 sequencing reads were trimmed to the expected gRNA length by searching for known anchor sequences relative to the guide sequence using a custom python script (<https://github.com/hwessels/Cas13>). For the combinatorial pooled screen, we extracted the first 15 bases in read2. For the single gRNA pooled screen, we collapsed (FASTX-Toolkit v.0.0.14) processed reads to count duplicates followed by string-match intersection with the reference to retain only perfectly matching alignments (average mapping rate 82.3%, median gRNA count 167). For the combinatorial pooled screen, preprocessed reads were aligned to the barcode reference using bowtie⁴³ (v.1.1.2) with parameters -v 1 -m 1 -best -strata (average mapping rate 97%; median barcode read count 635; one barcode was not detected in input samples). For each dataset, raw counts were normalized using a median of ratios method as in DESeq2 (ref.⁴⁴) and batch corrected using combat implemented in SVA (v.3.34.0)⁴⁵. gRNA and bcgRNA enrichments were calculated building the count ratios between a sorting bin or timepoint and the indicated reference sample followed by log₂-transformation (log₂FC). For every gRNA or bcgRNA, we considered the mean log₂FC across replicates. For the single gRNA pooled screen, we used the four best performing gRNAs per target gene to calculate the mean log₂FC, where we determined best as either highest or lowest dependent on the sign of the mean enrichment across all

ten gRNAs. As we have previously described¹¹, we noticed that log₂FC enrichments were generally more pronounced in samples using the enhanced direct repeat. Consistency between replicates and selected gRNAs was estimated using Robust Rank Aggregation (v.1.1)⁴⁶. For the combinatorial pooled screen, we calculated the mean of both replicate arrays per gene pair. We noticed GFI1 g2 did not lead to strong effects in the pooled screen and in the CaRPool-seq experiment. The technical replicate arrays including GFI1 g2 were removed in all analyses. Enrichments are available in Supplementary Tables 4 and 5 (*P* values derived from Robust Rank Aggregation).

Direct capture Perturb-seq

Monoclonal CRISPR–Cas effector protein-expressing cell lines (Cas9-nuclease, KRAB–dCas9, KRAB–dCas9–MeCP2) were infected with one of six sgRNA pools (KO-1, KO-2, KO-3 or CRISPRi-1, CRISPRi-2 and CRISPRi-3) (Supplementary Table 1), providing 1–3 sgRNAs in a single vector and a total of nine cell line pool combinations. Cell survival after selection ranged between 1.7 and 5.5% (MOI < 0.1) assuring a high single integration probability. Viral titers were confirmed by measuring the fraction of BFP-positive cells for pools that have received vectors carrying 2+ sgRNAs using flow cytometry. Cells were passaged every 2–3 days (replenishing puromycin and blasticidin at each split) maintaining high sgRNA representation (>1,000× coverage). We confirmed that >98% of cells were BFP-positive before the 10X experiment. We performed 10X (Chromium Single Cell 3' Gene Expression v3 with Feature Barcoding technology for CRISPR screening, nos. 1000074, 1000075 and 1000079) 12 days posttransduction. Cells were stained with a pool of five TotalSeq-A antibodies (0.75 µg per antibody per 2 × 10⁶ cells) (Supplementary Table 6) following the CITE-seq protocol¹². In addition, we used Cell hashing²² (Supplementary Table 7) to track the nine cell line pool combinations. Before the run, cell viability was determined (≥96%). We ran one 10X lane, leveraging our hashed experimental design loading 38,600 cells. mRNA, sgRNA feature, hashtags (hashtag-derived oligos, HTOs), protein (Antibody-derived oligos, ADTs) libraries were constructed by following 10X Genomics Cell hashing and CITE-seq protocols^{12,22}. All libraries were sequenced together on one NextSeq 75 cycle high-output run.

Direct capture Perturb-seq analysis

Gene expression data was mapped to the hg38 (ensembl v.97) genome reference using Cellranger (v.3.0.1). Guide RNA reads were mapped simultaneously to a sgRNA feature reference (Supplementary Table 1). Before feature mapping, we performed 5' adapter trimming using cutadapt to account for varying lengths of poly-G tracks five prime to the sgRNA feature (first -g AAGCAGTGGTATCAACGCAGAGTACAT -O 5; then -O 1 -e 0 -g XGGGGGGGGGG) and trimmed the resulting reads to a length of 18 bases. We used CITE-seq-count package (v.1.4.2) for HTO and ADT quantification. Count matrices were then used as input into the Seurat R package (v.4.0)⁴⁷ to perform downstream analyses. We detected 16,842 cells. HTO and sgRNA counts were normalized using the centered log-ratio transformation approach (margin of 2). To assign experimental conditions and remove cell doublets, we used the HTODemux function in Seurat, with default parameters.

For sgRNA assignment, we customized HTODemux to return identities of second and third sgRNA without changing the underlying modeling approach. We flagged cells with an incorrect number of expected sgRNAs based on the HTO pool assignment. Furthermore, we flagged cells with an unexpected combination of sgRNAs not present in the sgRNA pool used to transduce the cells.

For the analysis shown in Fig. 3, we only retained cells with the correct sgRNA numbers and identities. ADT counts were log-normalized, before running ScaleData (do.scale=FALSE, vars.to.regress=Perturb-Seq.approach). PCA was performed on normalized ADT counts using all five features, followed by uniform manifold approximation and projection (UMAP) dimensional reduction using

four dimensions. To compare target knockdown across Perturb-seq approaches for NT cell and cells that received all three (sg)RNAs (CD46, CD55, CD71), we normalized cellular ADT counts using median of ratios across ADT features that were not targeted (CD29, CD56) to derive a scaling factor per cell, and divided the normalized ADT counts by the mean ADT counts in NT cells for each Perturb-seq approach.

CaRPool-seq experiments

We transduced and treated Cas13d-NLS expressing HEK293FT, NIH/3T3 or THP1 cells as described in the Supplementary Information. In the species mixing, we used a pool of three bcgRNAs per species together with NT gRNAs. The HEK293FT CaRPool-seq experiment included 29 CRISPR arrays (Supplementary Table 1) barcoding a diverse set of array configurations around four gRNAs that allowed us to assess gRNA positioning within the CRISPR array, effects of the relative gRNA amount per cell and combinatorial targeting of multiple RNA transcripts. CaRPool-seq species mixing and CaRPool-seq were conducted simultaneously in one lane of 10X Genomics 3' kit. CaRPool-seq was performed on THP1 cells 5 days post-Cas13d induction (1 µg ml⁻¹ Doxycycline) using four lanes of a 10X Genomics 3' kit. THP1 CaRPool-seq library design and cloning were described above. Before the runs, cell viability was determined ≥95% for each experiment.

The HEK293FT CaRPool-seq experiment was stained with a pool of five TotalSeq-A antibodies (0.75 µg per antibody per 2 × 10⁶ cells) (Supplementary Table 6) as following the CITE-seq protocol¹². Similarly, THP1 cells were first treated with FcX-blocking buffer (BioLegend no. 422302, 10 min at room temperature), before staining cells with a pool of 22 TotalSeq-A antibodies (Supplementary Table 6). To keep track of the experiment identity and identify multiplets, samples were hashed (subsequent to CITE-seq antibody staining) (Supplementary Table 7) following the Cell Hashing protocol²². mRNA, hashtags (HTOs), protein (Antibody-derived oligos, ADTs) libraries were constructed by following 10X Genomics Cell hashing and CITE-seq protocols^{12,22}.

Species mixing and HEK293FT CaRPool-seq experiment libraries were sequenced together on one NextSeq 75 cycle high-output run. THP1 CaRPool-seq libraries were sequenced on NovaSeq6000 using the XP S4 2 × 100 v.1.5 workflow. Sequencing reads coming from the mRNA library were mapped to a joined genome reference of hg38 (ensemble v.97) and mm10 using the Cellranger Software (v.3.0.1), or to hg38 using Cellranger v.6.0.0 for the THP1 experiment. bcgRNA library reads were mapped simultaneously to a barcode reference (Supplementary Table 1) using Cellranger. To generate count matrices for HTO and ADT libraries, the CITE-seq-count package (v.1.4.2) was used (<https://github.com/Hoohm/CITE-seq-Count>). Count matrices were then used as input into the Seurat R package (v.4.0)⁴⁷ to perform all downstream analyses.

CaRPool-seq library preparation

We used Cas13 CRISPR array configurations of type X (Fig. 1a and Extended Data Fig. 2). Specifically, the bcgRNA was placed in the last array position and entailed a spacer sequence composed of a five-prime Illumina small RNA PCR handle, a 15mer barcode and a three-prime capture sequence 1 (CS1) compatible with 10X Genomics feature barcoding. This composition allowed the specific amplification of a bcgRNA amplicon with a unique combination of forward and reverse primers. Moreover, usage of the Illumina 5' PCR handle allows for efficient sequencing of the bcgRNA amplicon with the first base of read2 being the first barcode base. In our last experiment (Fig. 5), we added structured RNA elements 3' to the CS1 sequence.

CaRPool-seq experiments were conducted using the 10X Genomics 3' kit (Chromium Single Cell 3' Gene Expression v3 with feature barcoding technology for CRISPR screening, nos. 1000074, 1000075 and 1000079). Library construction for bcgRNA derived oligos is outlined in Extended Data Fig. 2 and largely followed 10X Genomics user guide CG000184 Rev C with some modifications. Specifically, we eluted the

GEM-RT in 33 μ l and added 2 μ l containing 0.4 μ M ADT additive primer (for bcgRNAs and ADTs) and 0.2 μ M HTO additive primer before complementary DNA amplification. The cDNA was purified using 0.6 \times SPRI cleanup for mRNA fraction. The supernatant containing ADT, HTO and bcgRNA cDNA was purified by adding another 1.4 \times SPRI (0.6 + 1.4 = 2 \times SPRI) followed by a second 2 \times SPRI cleanup. The purified short fragments were split into three pools (for example, 3 \times 20 μ l). One pool each was used for HTO and ADT library construction as described before^{12,22}. Half of the remaining pool (10 μ l) was used to construct the bcgRNA library using two PCR recipes. PCR1 adds Illumina P5 and P7 handles to the bcgRNA amplicon (100 μ l of PCR1: 50 μ l of 2 \times KAPA Hifi PCR Mastermix, up to 45 μ l of bcgRNA PCR template, 2.5 μ l of Feature SI Primers 210 μ M, 2.5 μ l of TruSeq Small-RNA RPIx primer (containing i7 index) 10 μ M; 95 $^{\circ}$ C 3 min, 12 \times (95 $^{\circ}$ C 20 s, 60 $^{\circ}$ C 8 s, 72 $^{\circ}$ C 8 s), 72 $^{\circ}$ C 1 min). The 1.6 \times SPRI-purified PCR1 product was amplified in PCR2 (100 μ l: 50 μ l of 2 \times KAPA Hifi PCR Mastermix, up to 45 μ l of PCR1 product, 2.5 μ l of P5 primer 10 μ M, 2.5 μ l of P7 primer 10 μ M; 95 $^{\circ}$ C 3 min, 4 \times (95 $^{\circ}$ C 20 s, 60 $^{\circ}$ C 8 s, 72 $^{\circ}$ C 8 s), 72 $^{\circ}$ C 1 min). The final bcgRNA amplicon (203 bp) can be sequenced with standard Illumina sequencing primers (\geq 28 cycles read1 and \geq 15 cycles read2) (Extended Data Figs. 2 and 3a).

CaRPool-seq data analysis

Cells from species-mixing and HEK293FT CaRPool-seq experiments were processed together. Cells with <2,500 UMI were removed. HTO and bcgRNA counts were normalized using the centered log-ratio transformation approach (margin of 2). We used HTODemux to identify cell doublets and assign experimental conditions. Only human cells were hashed, with mouse NIH/3T3 cells being the only cell population without a hashtag. We removed all hashing doublets within the CaRPool-CITE-seq experiment (HTO-01 to HTO-08) and to human cells in the species-mixing experiment (HTO-10). In addition, we removed all cells labeled with a single HTO-01 to HTO-08 if the fraction of mouse reads was >10%, and cells without any HTO if not at least 10% mouse reads were present. Like this, we removed all doublets between CaRPool-seq species mixing and CaRPool-CITE-seq experiments while retaining potential collisions/doublets within the species-mixing experiment. At this point, the experiment was split into two separate objects. For the species-mixing experiment, we determined species identity by quantifying the fraction of human reads for RNA and for the species-specific bcgRNAs (human >0.9, mouse <0.1, collision 0.9 to 0.1). For the HEK293FT CaRPool-CITE-seq experiment RNA counts were log-normalized using the standard Seurat workflow after removing all mouse features and RNA counts. bcgRNA identity was determined using MultiSeqDemux (autoThresh=T). Cells without a bcgRNA assigned and cells with multiple bcgRNA assignments were removed. Differential expression analyses were done using FindMarkers (Wilcoxon's rank-sum test, pseudocount.use of 1×10^{-4}). We converted log₂ fold changes to percent knockdown for each target gene in each of the 26 targeting conditions and took the mean to calculate the average target knockdown,

For the THPI experiment we detected 52,496 single cells (nFeature_RNA > 1,000, nFeature_RNA < 8,000, percent.mt < 20) after HTO demultiplexing using HTODemux as described above. Model-based bcgRNA assignments (HTODemux or MultiSeqDemux) did not yield satisfying results supported by the observed phenotypic changes, likely due to model limitations imposed by the high number of bcgRNA features. Instead, we assigned bcgRNAs to single cells by applying the following rules: We compared UMI counts for the bcgRNA with the highest UMI count (g1) to, if present, the second detected bcgRNA (g2). bcgRNA counts for g2 may derive from spurious counts arising from library preparation, or from integration of more than one viral element (bcgRNA multiplet). We considered cells with g1 < 5 as negative. We assigned g1 if: (1) g1 = (5–9) and g2 = (0–1) or (2) g1 > 9 and g1/(g1 + g2) > 0.8 and g2 < 11. All other cells were considered bcgRNA multiplets. We assigned 31,308 with a single bcgRNA. Comparing

differential gene expression results for technical replicates embedded in the CaRPool-seq library, we noticed GF11 g2 did not lead to upregulation of CD11b ADT or upregulation of the expected gene expression signature. We removed all cells with GF11 g2 ($n = 601$).

Changes in cell surface protein ADT levels for gene pair or individual CRISPR array were calculated using Wilcoxon's rank-sum test in FindMarkers relative to NT control cells. Changes were determined by repeating the differential expression analysis ten times with \leq 30 randomly samples cells per cell group to account for differing numbers of cells followed by averaging. We compared differential CD11b expression between single and dual perturbations by comparing the log₂-transformed fold changes of dually perturbed cells to the log₂-transformed mean fold changes of the two single-gene perturbations.

Cas13d gRNA off-target evaluation

To identify potential Cas13d gRNA off-target binding sites we aligned gRNAs to the human transcriptome (GRCh38 cdna.all and noncoding RNA from emsembl release 97) using blastn (v.2.6.0) (megablast) with the following parameters (-strand minus -max_target_seqs 10,000 -evalue 10,000 -word_size 5 -perc_identity 0.7). Second, candidates were further filtered to match with at least 17 bases, as shorter matches do not lead to target knockdown and show a blastn e.value of <100. In Extended Data Fig. 4a, we demonstrate that despite the potential for off-target binding, we do not observe transcriptomic perturbation for these genes.

Cas13d collateral activity was evaluated by comparing expression levels of mitochondrial genes¹⁵ in cells expressing targeting gRNAs versus NT gRNAs using FindMarkers (Wilcoxon's rank-sum test, pseudocount.use 1×10^{-4}). To assess differences in cell fitness, we classified single-cell transcriptomes into gene expression programs usually observed at different cell cycle stages (Seurat's CellCycleScoring), and compared the distribution of cells per cell cycle stages between groups of cells.

Modeling of genetic interactions in single-cell data

To decompose transcriptomic profiles of double perturbation, we used a linear regression model as previously introduced⁷ and implemented it in R. First, we z-scaled the log-normalized gene expression counts for all cells with respect to the mean and standard deviation of the control group (NT cells). In this way, we have subtracted the baseline expression profiles from each cell and can directly compare the deviation from each perturbation to NT conditions. Next, we grouped cells by gene pair and calculated pseudobulk z-scaled profiles (single perturbations (a, b), and double perturbation (ab)) by calculating the mean across cells for each feature. The average NT-cell profile returns a vector of all zeros. We generated average profiles for 1,530 genes with an average UMI count >0.5. We included gene pairs when all cell groups were represented by at least 25 cells (Examples in Fig. 4g and Extended Data Fig. 8d–h).

As previously introduced⁷, we model the average z-scale profiles using:

$$\delta ab = c_1 \delta a + c_2 \delta b + \epsilon$$

with δa and δb being the pseudobulk z-scaled profile for cells assigned to single perturbations **a** and **b**, respectively, while δab is the pseudobulk z-scaled profile for cells assigned to double perturbation **ab**. c_1 and c_2 are constants fitted to the data indicating the relative weight of δa and δb profiles. The vector ϵ collects the residuals to the model fit. In our plots, **a** is the first gene in the gene pair and **b** is the second gene. c_1 corresponds to **a**, and c_2 to **b**.

We implemented the previously introduced model-fitting procedure⁷, using the rlm function from the MASS package (v.7.3-58.1), and extracted the mean coefficients (c_1 and c_2) and residual error ϵ . We collected six measures to evaluate the fit as described before⁷ (dcor function in energy package v.1.7-10):

Model fit: $dcor(c_1\mathbf{a} + c_2\mathbf{a}, \mathbf{ab})$

Dominance: $|\log_{10}(c_1/c_2)|$

Magnitude: $(c_1^2 + c_2^2)^{1/2}$

Similarity of single to double profiles: $dcor((\mathbf{a}, \mathbf{b}), \mathbf{ab})$

Similarity of single profiles: $dcor(\mathbf{a}, \mathbf{b})$

Equality of contribution: $\min(dcor(\mathbf{a}, \mathbf{ab}), dcor(\mathbf{b}, \mathbf{ab}))/\max(dcor(\mathbf{a}, \mathbf{ab}), dcor(\mathbf{b}, \mathbf{ab}))$

Each feature and its interpretation are described in detail in ref. ⁷. Features were scaled (margin of 2) before hierarchical clustering (dist, euclidean; methods, ward) to generate a dendrogram, shown in Fig. 4g. For clarity, the heatmap in Fig. 4g shows unscaled values.

The example interactions shown in Fig. 4h and Extended Data Fig. 8d–h depict the union of top 20 differentially expressed genes for each cell group (\mathbf{a}, \mathbf{ab}) relative to NT cells (selected by *P* value) derived using the Wilcoxon's rank-sum test in FindMarkers. Model prediction and residuals are derived from the modeling approach described above. The color scale represents the average z-score normalized expression per gene pair.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

Raw and processed sequencing data have been made available on the National Center for Biotechnology Information Gene Expression Omnibus under the accession number [GSE213957](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE213957). ECCITE-seq data used in this study are available at the Gene Expression Omnibus ([GSE146469](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE146469), ref. ²³). Source data are provided with this paper.

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Acknowledgements

We thank the Technology Innovation laboratory as well as all members of the Sanjana and Satija laboratories for helpful discussions. We are

grateful to Z. Daniloski for cloning the Cas9-effector protein plasmids, to I. Aifantis for advice and helpful discussion related to THP1 experiments, and the Technology Innovation laboratory for generously sharing CITE-seq reagents. N.E.S. and R.S. are supported by New York University and New York Genome Center startup funds. N.E.S. is further supported by DARPA (grant no. D18APO0053), the Brain and Behavior Foundation, the Cancer Research Institute, the National Institutes of Health (NIH)/National Human Genome Research Institute (grant no. DP2HG010099) and the NIH/National Cancer Institute (grant no. R01CA218668). R.S. is supported by the Chan Zuckerberg Initiative (grant nos. EOSS-0000000082 to R.S., HCA-A-1704-01895 to P.S. and R.S.), and the National Institutes of Health (grant nos. DP2HG009623-01 to R.S. and RM1HG011014-01 to P.S. and R.S.).

Author contributions

H.-H.W., N.E.S. and R.S. conceived the research. R.S. and N.E.S. supervised the research. H.-H.W. and A.M.-M. performed experimental work, assisted by E.P., W.M.M. and L.L. E.P.M. and P.S. advised with bcgRNA design. H.-H.W. performed computational analysis. Y.H. performed integration and pseudotime analysis. J.A.M. validated dCas9-effector constructs. All authors participated in data interpretation. H.-H.W., N.E.S. and R.S. wrote the manuscript with input from all authors. All authors read and approved the final manuscript.

Competing interests

In the past 3 years, R.S. has worked as a consultant for Bristol-Myers Squibb, Regeneron and Kallyope, and served as a SAB member for ImmunAI, Apollo Life Sciences GmbH, Nanostring and the New York City Pandemic Response Laboratory. N.E.S. is an advisor to Vertex and QIAGEN and is a cofounder of OverT Bio. P.S. is a coinventor on a patent related to protein detection by sequencing as described in this work. The New York Genome Center and New York University have applied for patents relating to the work in this article. The remaining authors declare no competing interests.

Additional information

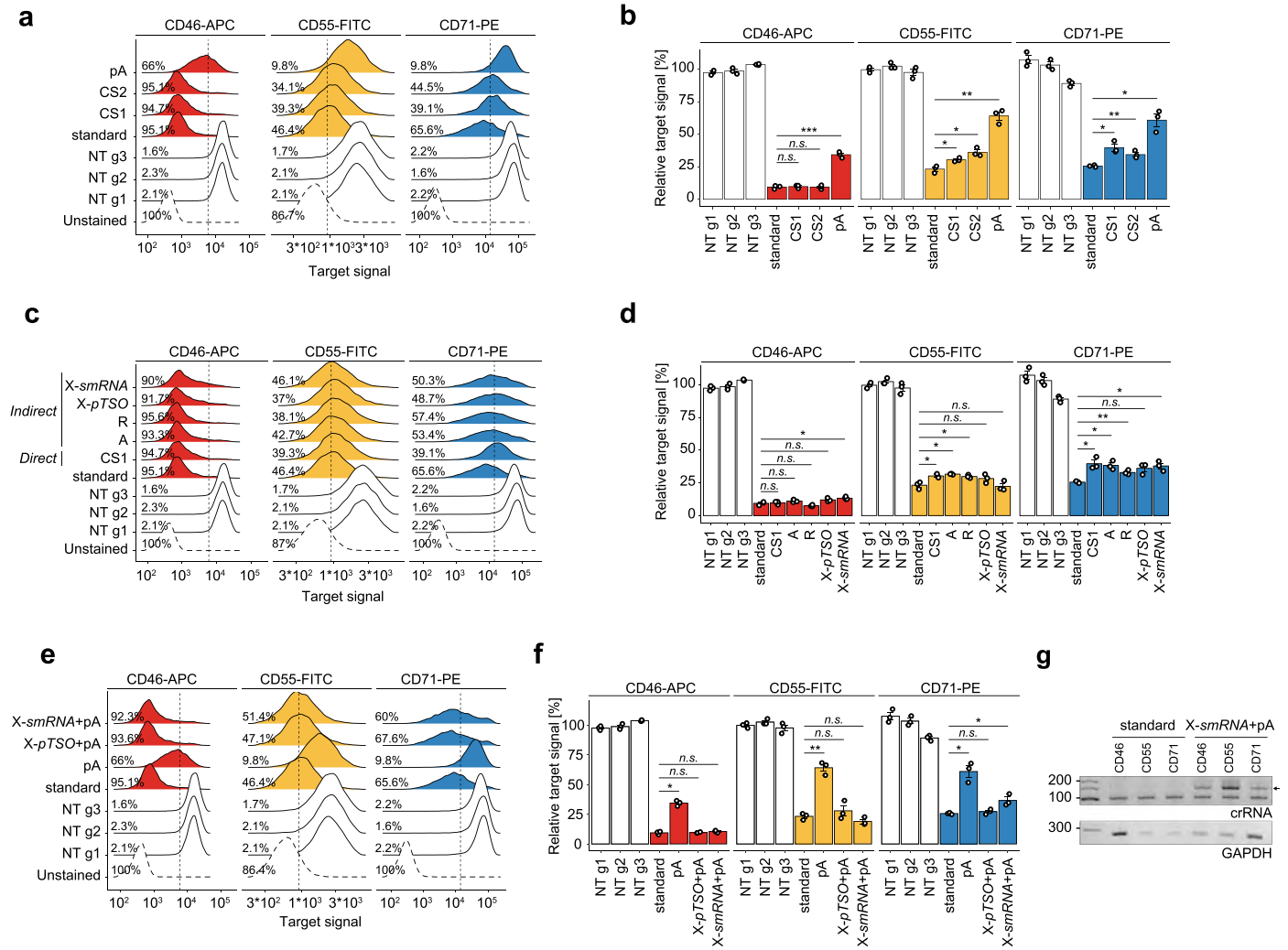
Extended data is available for this paper at <https://doi.org/10.1038/s41592-022-01705-x>.

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41592-022-01705-x>.

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Peer review information *Nature Methods* thanks the anonymous reviewers for their contribution to the peer review of this work. Primary Handling Editor: Lei Tang, in collaboration with the *Nature Methods* team.

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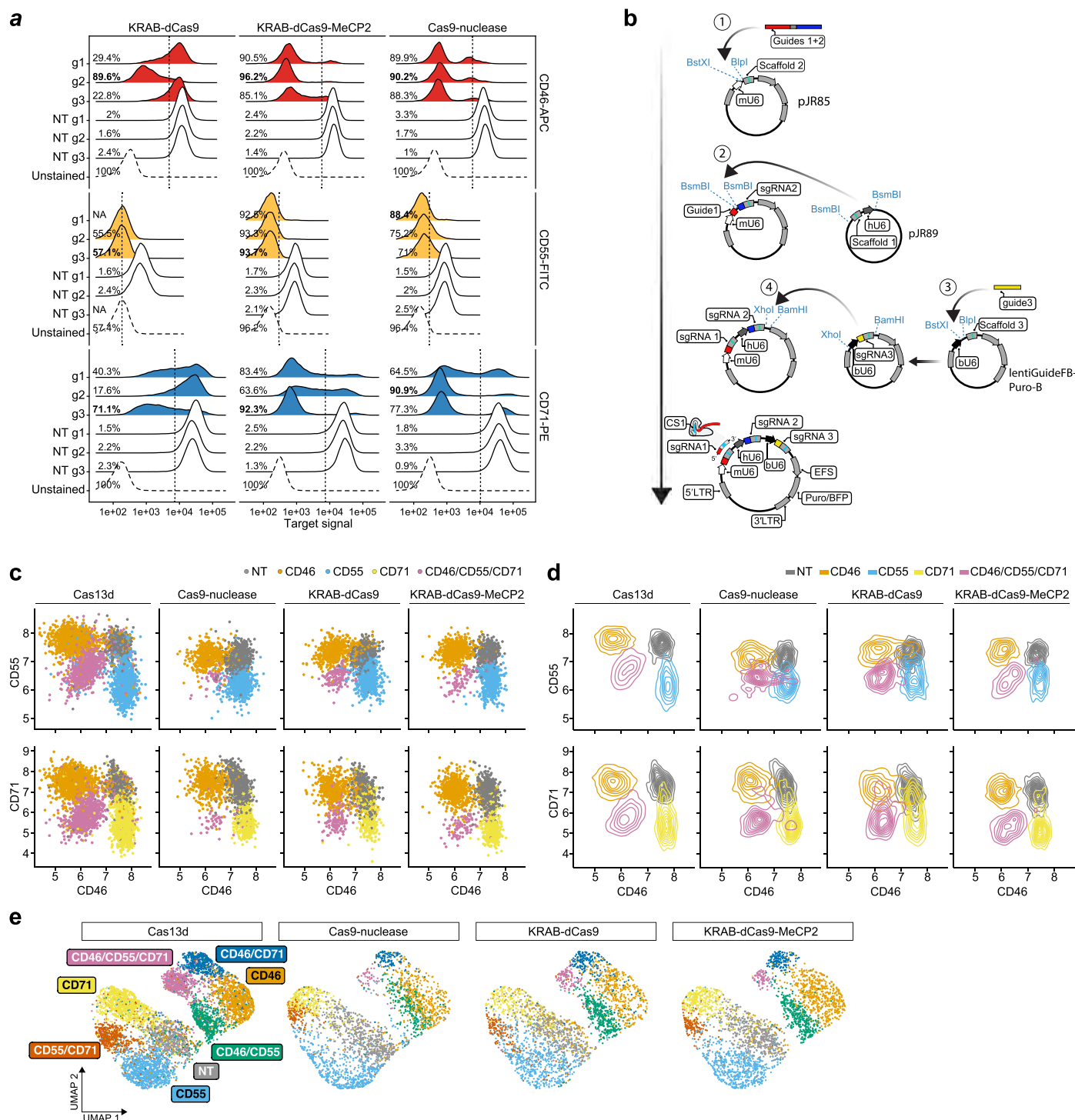


Extended Data Fig. 1 | Direct and indirect Cas13 guide RNA capture allow for robust target knockdown. **a)** Density plots showing the CD46-APC, CD55-FITC and CD71-PE flow cytometry signal upon Cas13d-mediated knockdown with either regular gRNAs or a direct capture gRNA with one of three reverse transcription handles (pA(30) = polyA-tail of length 30, CS1 = 10x Genomics Capture Sequence 1, CS2 = 10x Genomics Capture Sequence 2, NT = non-targeting). Vertical lines mark the threshold for CD-protein negative cells (2nd percentile of NT cell populations), indicating the percent negative cells for one replicate experiment. Importantly, the Cas13-mediated function shows a unimodal response, suggesting limited cell-to-cell differences in target gene knockdown. N > 5000 cells examined per sample. Shown is one representative replicate. **b)** Summary analysis of biological replicate experiments (n = 3) as shown in (a). Y-axis shows the mean fluorescent intensity (MFI) relative to the average of all NT cell populations. Direct capture constructs with CS1 or CS2 enable strong knockdown for CD46, but reduced knockdown for CD55 and CD71. Direct capture with pA-handle shows strongly reduced knockdown efficiency compared to regular gRNAs (standard condition). Two-sided t-test with * p < 0.05, ** p < 0.01, and *** p < 0.001. Error bars depict SEM. **c)** Density plots showing the CD46-APC, CD55-FITC, and CD71-PE signal upon Cas13d-mediated knockdown with either regular gRNAs, a direct capture gRNA, or indirect capture construct of types A, R, and X as shown in Fig. 1a. CS1 was used in all constructs with RT-handle. Type X was used with either a partial TSO (pTSO) PCR priming site or an Illumina smallRNA PCR-handle sequence. Vertical lines mark the threshold for CD-protein negative cells, indicating the percent negative cells for one replicate experiment. N > 5000 cells examined per sample. Shown is one representative replicate. **d)** Summary analysis of biological replicate experiments (n = 3) as

shown in (c). Y-axis shows the mean fluorescent intensity (MFI) relative to the average of all NT cell populations. Indirect capture constructs show strong target gene knockdown similar to regular gRNAs (standard condition) for all three target genes. The slight reduction in targeting efficiency in indirect guide capture may be explained by CRISPR array processing constraints. Two-sided t-test with * p < 0.05, ** p < 0.01, and *** p < 0.001. Error bars depict SEM. **e)** Density plots showing the CD46-APC, CD55-FITC, and CD71-PE signal upon Cas13d-mediated knockdown with either regular gRNAs, a direct capture gRNA, or indirect capture construct of type X. Here, comparing the effect and placement of a polyA-tail RT-handle. pA indicates direct capture construct with polyA-tail. Type X was used with either a pTSO or smallRNA PCR-handle sequence. Vertical lines mark the threshold for CD-protein negative cells, indicating the percent negative cells for one replicate experiment. N > 5000 cells examined per sample. Shown is one representative replicate. **f)** Summary analysis of biological replicate experiments (n = 3) as shown in (e). Y-axis shows the mean fluorescent intensity (MFI) relative to the average of all NT cell populations. Indirect capture constructs show strong target gene knockdown like regular gRNAs (standard condition) for all three target genes. Target knockdown with direct capture through a polyA-tail sequence is limited. Two-sided t-test with * p < 0.05, ** p < 0.01, and *** p < 0.001. Error bars depict SEM. **g)** PCR amplicons of reverse-transcribed crRNAs from lentivirally infected cells used in (e) showing one representative experiment. Indirect capture of Type-X crRNAs with smallRNA PCR-handle and polyA-tail (arrow) allowed for reverse transcription and amplification. These results show that indirect gRNA capture can be facilitated with polyA-tail capture as an alternative to CS1-based capture.

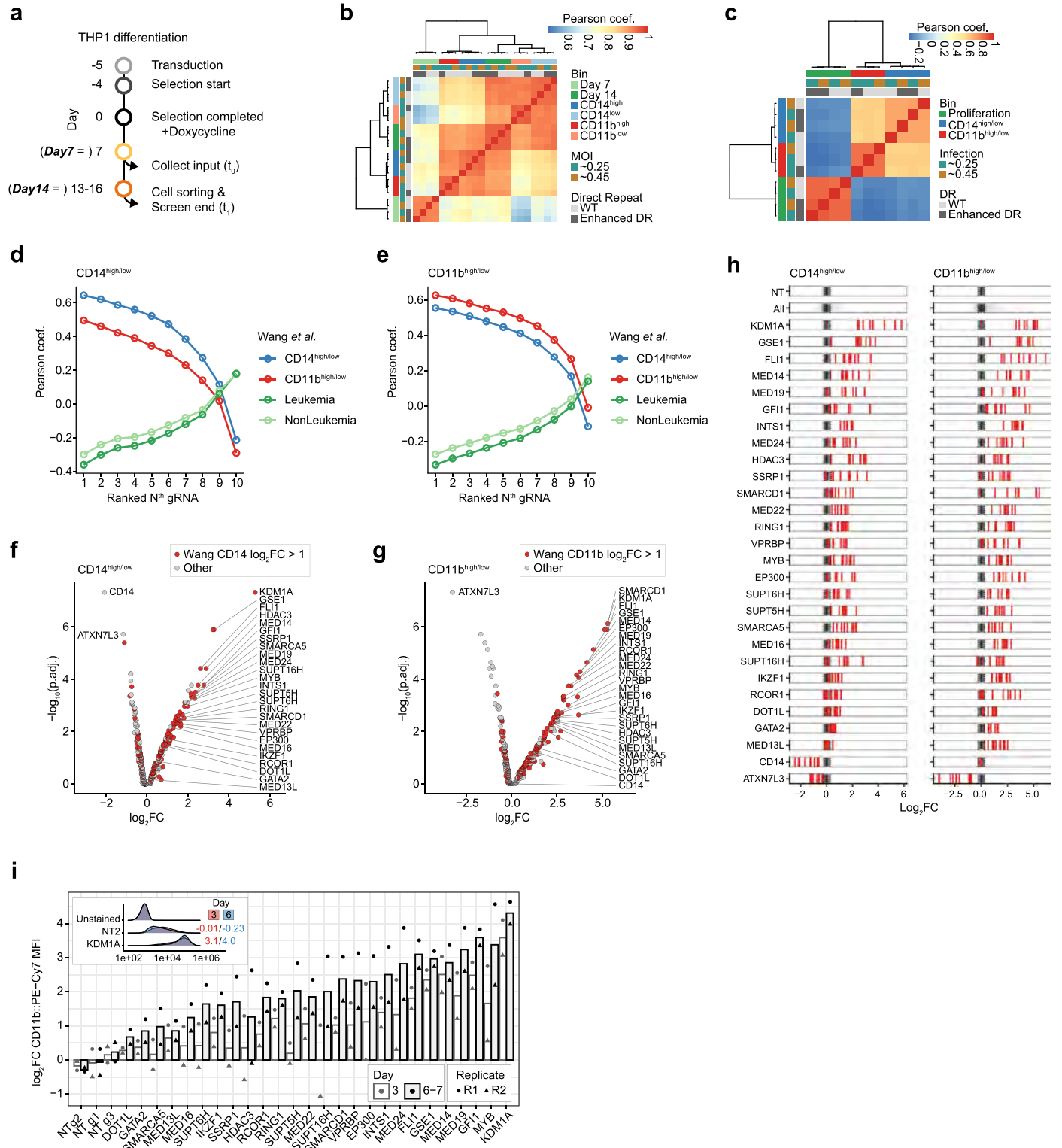
Extended Data Fig. 3 | CaRPool-seq enables efficient bcgRNA capture and specific target RNA knockdown. a) Representative BioAnalyzer traces of cDNA and four jointly assayed modalities (GEX = gene expression, bcgRNA = barcode guide RNA, ADT = antibody derived tags, HTO = hashtag oligonucleotides). **b)** Stacked violin plot showing normalized bcgRNA UMI counts for cells grouped by assigned CRISPR array [total cells $n = 9,355$, cells with single bcgRNA $n = 6,986$, (74.7%), $n = 29$ single bcgRNA conditions; median number of cells 269 per condition, s.d. 97 cells]. **c)** Bar plots depicting CD46-APC, CD55-FITC, and CD71-PE signal upon Cas13d-mediated knockdown with three alternative gRNAs per target gene relative to the mean of three NT controls measured by flow cytometry. Y-axis shows the mean fluorescent intensity (MFI) relative to the average of all NT cell populations. Two-sided t-test with * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$. ($N = 3$ replicate experiments; error bars depict SEM). Guide RNA g1 was used in CaRPool-seq experiments. Guide RNAs g2 and g3 are used in figures (d) and (e). **d)** Density plots showing the CD46-APC, CD55-FITC, and CD71-PE signal upon Cas13d-mediated knockdown with either 1, 2, or 3 copies of the same gRNA (g1) per CRISPR array or 2 and 3 alternative gRNAs (g2, g3). Vertical lines mark the threshold (2nd percentile of combined NT conditions) for CD-protein negative cells, indicating the percent negative cells for one replicate experiment. $N > 5000$ cells examined per sample. Shown is one representative replicate. **e)** Summary analysis of biological replicate experiments ($n = 3$) as shown in

(d). Y-axis shows the mean fluorescent intensity (MFI) relative to the average of all NT cell populations. The Analysis suggests that target gene knockdown differences between the number of gRNAs per array are more pronounced than differences between gRNA identities with the same total gRNA count, given that gRNA efficiencies are comparable as shown in (c). CRISPR arrays encoding multiple gRNAs against the same target may be used to further enhance target knockdown. Two-sided t-test with * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$. Error bars depict SEM. **f)** Scatterplots showing normalized pseudobulk RNA UMI count profiles of cells grouped by indicated CRISPR arrays (y-axis) and control cells that received non-targeting (NT) gRNAs (x-axis). Respective target genes (CD46, CD55, CD71) are highlighted in color. Genes on the MT chromosome are colored green. Other significantly differentially regulated genes (Wilcoxon's rank sum test; adjusted p-value < 0.05) are highlighted in black. Genes highlighted in black showed a median expression change of 12.8% (s.d. 9.9%). CD71 + CD71 was not included in the experiment. **g)** Volcano plots showing differential gene expression results cells grouped by indicated CRISPR arrays and control NT cells. Cells grouping is the same as in (f). The x-axis indicates log₂-transformed fold changes. The y-axis depicts -log₁₀-transformed adjusted p-values (Wilcoxon's rank sum test). Significantly differentially regulated genes (adjusted p-value < 0.05) are highlighted in red.



Extended Data Fig. 5 | Comparison of CaRPool-seq to alternative combinatorial perturbation approaches. a) Density plots showing the CD46-APC, CD55-FITC, and CD71-PE flow cytometry signal upon Cas9-nuclease mediated knockout (KO) and CRISPRi-mediated (KRAB-dCas9, KRAB-dCas9-MeCP2) knockdown with three alternative sgRNAs from established genome-wide KO20 and CRISPRi21 libraries. Vertical lines mark the threshold (2nd percentile of combined NT conditions) for CD-protein negative cells, indicating the percent negative cells for one replicate experiment. Single guide RNAs with the highest percentage of negative cells (bold) were selected for direct capture Perturb-seq experiments (NA = sgRNA not assayed). **b)** Cloning strategy for triple sgRNA plasmid vectors. Dual sgRNA constructs were cloned as described before

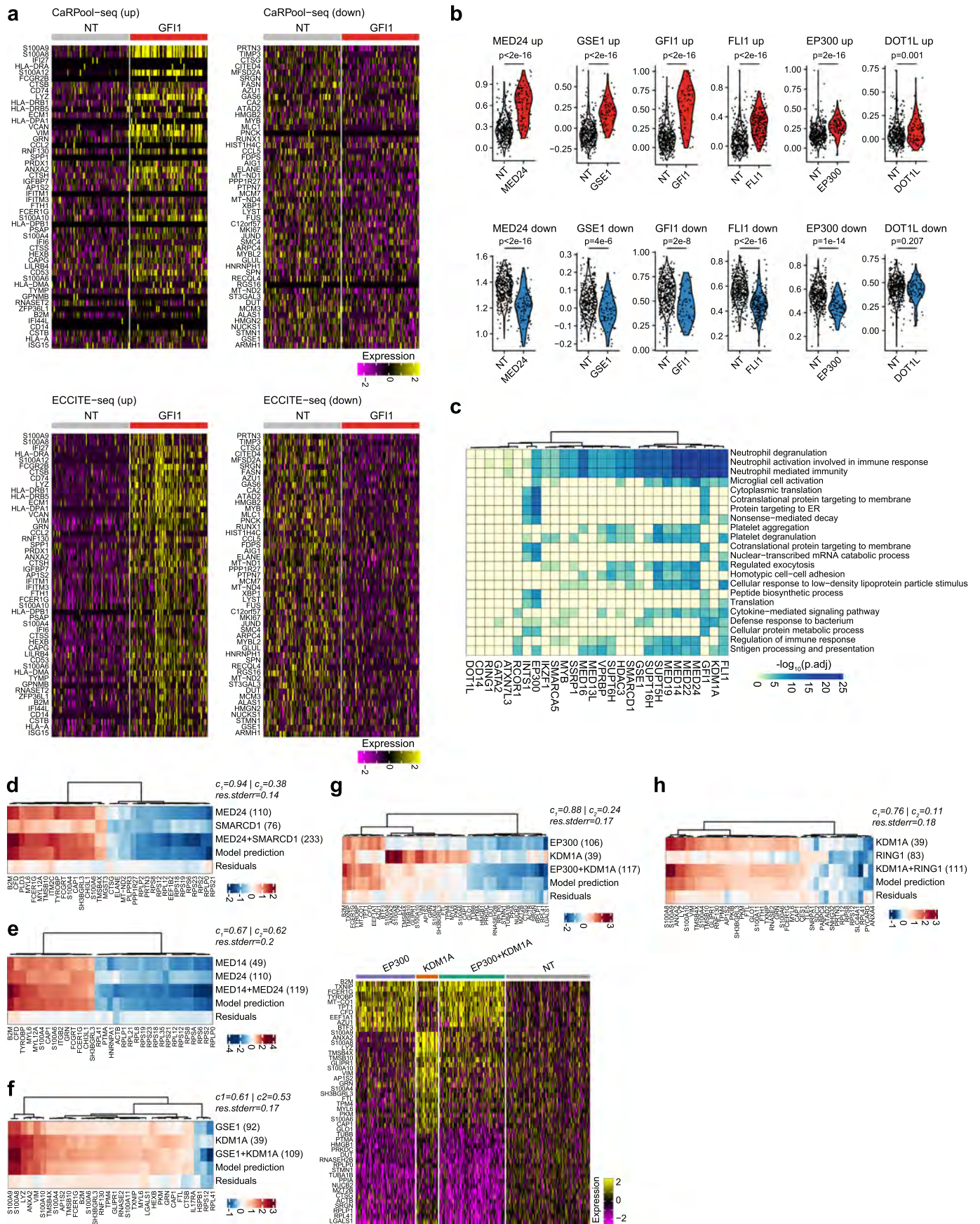
6. The third sgRNA was cloned behind a bovine U6 promoter using an alternative sgRNA scaffold tested before **c)** Cell surface protein expression (log₂-normalized UMI counts) of CD46, CD55 and CD71 in cells assigned with indicated (s)gRNAs. CaRPool-CITE-seq (n = 4,979 cells) and Perturb-seq experiments using Cas9-nuclease (n = 2,270), KRAB-dCas9 (n = 2,104) or KRAB-dCas9-MeCP2 (n = 2,326). **d)** Contour plots of data shown in (c). **e)** Protein level ADT-based clustering of single-cell expression profiles of merged CaRPool-CITE-seq (n = 6,986 cells) and Perturb-seq experiments using Cas9-nuclease (n = 2,836), KRAB-dCas9 (n = 2,911) or KRAB-dCas9-MeCP2 (n = 3,038) effector proteins as in Fig. 3e. Cells are labelled by the assigned target gene combination based on detected bcgRNA or sgRNAs and split by Perturb-seq.



Extended Data Fig. 6 | See next page for caption.

Extended Data Fig. 6 | A pooled Cas13 screen identifies regulators of AML differentiation. **a)** Timeline for THP1 cell infections and pooled screen readouts for CD14 and CD11b fluorescent activated cell sorting (FACS). We transduced a pooled lentivirus library with 4,800 gRNAs targeting 439 genes (10 gRNAs per gene) and 410 NT control gRNAs. Each gRNA was tested using two alternative Cas13d direct repeat (DR) sequences [wildtype (WT) or enhanced DR; see Methods]. Cells were infected at two different MOIs for each DR. Cells were collected at day 7 (timepoint 0; t0) and approximately day 14 (range between day 14 and day 16; t1) post Cas13d induction. On day 14, cells were sorted based on their cell surface protein expression into CD14 and CD11b high (top 15%) and low (bottom 15%) bins. At each time point, we collected and sorted cell populations with >1000x coverage. With alternative MOI infections and DR sequences used, we conducted four and three replicated phenotypic cell sorts for CD14 and CD11b. **b)** Pearson correlation of normalized and batch corrected gRNA counts for all samples. **c)** Pearson correlation of log2-transformed gRNA enrichments of the population of interest relative to the corresponding control population (CD11bhigh/low: gRNA counts in CD11bhigh bin divided by CD11blow bin; CD14high/low: gRNA counts in CD14high bin divided by CD14low bin; proliferation: gRNA counts at t1 divided by t0). **d)** Correlation of log2FC gene enrichments for CD14 upregulation (CD14high/low) to enrichments presented in Wang et al. Correlation analysis was repeated for every single ranked gRNA (see Methods), always considering only one ranked gRNA per target gene. This analysis indicated that, as expected, target gene enrichments for CD14 upregulation correlated best with CD14 target gene enrichments in Wang et al., and that correlations were similarly high for the top-ranked 4-5

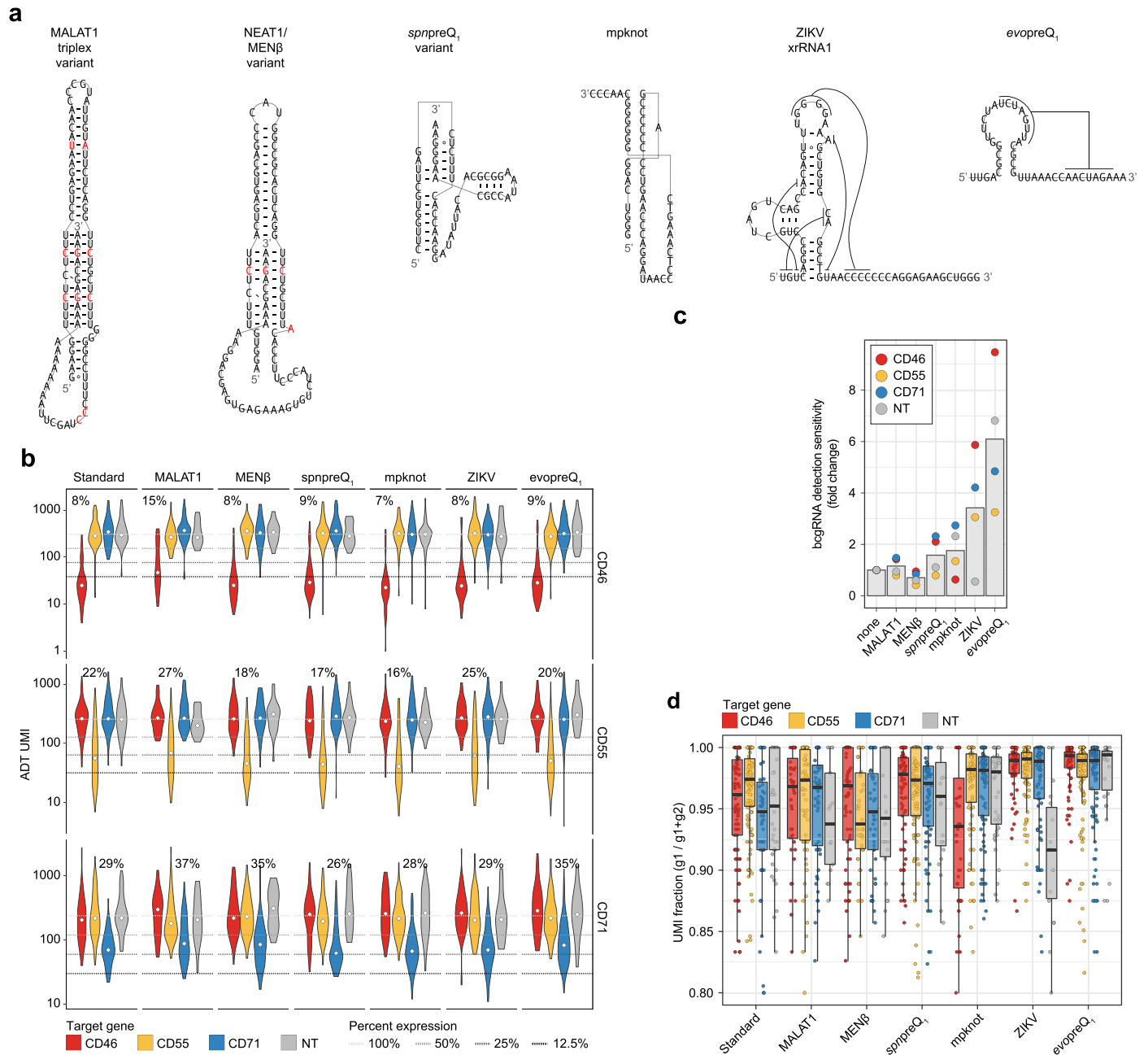
gRNA. **e)** Similar analysis as presented in d showing result for target genes regulating CD11b enrichments. **f)** Volcano plot showing gene enrichments for target genes regulating CD14 upregulation (CD14high/low). Each gene is represented as the mean of the four top-ranked gRNAs across all replicate experiments (see Methods). Y-axis shows $-\log_{10}$ transformed adjusted p-value derived from Robust Ranked Aggregation (RRA). Target genes selected based on previous results (Wang et al.) are shown in red. The 28 genes used in the subsequent CaRPool-seq experiment are highlighted. As expected, CD14 was the most depleted gene. **g)** Similar analysis as presented in (f) showing results for target genes that lead to CD11b enrichment. CD11b-targeting gRNAs were not included in the gRNA library. **h)** Consistent gRNA enrichment/depletion of all 28 target genes. (NT = all non-targeting gRNAs, All = all gRNAs, Gene Name = Red ticks highlighting targeting specific gRNAs atop of the non-targeting gRNA distribution (n = 10 per target gene). Dotted lines indicate the 95 percent confidence interval for NT gRNA distribution). **i)** CD11b expression upon individual gRNA infections for 26 hit genes and three NT controls. Cas13d expressing THP1 cells were transduced with individual gRNA-delivering lentivirus targeting one out of 26 selected target genes (gRNA was selected from pooled screen). Cells were assayed repeatedly (three and six-to-seven days post Cas13d-induction with doxycycline) for CD11b levels. Y-axis shows the CD11b::PE-Cy7 MFI relative to the average of all three NT control samples for the respective time point. Bars show the mean of two independent replicates (two THP1 Cas13d cell thaws infected on separate days). The inset shows CD11b::PE-Cy7 levels in KDM1A and NT targeted cells three and six days after Cas13d induction.



Extended Data Fig. 8 | See next page for caption.

Extended Data Fig. 8 | Transcriptome analysis of combinatorial targeting of AML differentiation regulators. a) Single-cell gene expression heatmap showing the 50 most up-regulated (left) and down-regulated (right) genes upon GF11 perturbation (Wilcoxon's rank sum test) identified in ECCITE-seq data (Wang et al.). We compared cells expressing non-targeting control gRNAs (NT) and GF11 targeting gRNAs for CaRPool-seq (top) and ECCITE-seq (bottom), respectively. The ECCITE-seq data was filtered using mixscape (Papalexi et al. 9) to remove unperturbed cells prior to identification of the most regulated genes. **b)** Gene module scores for the 50 most up-regulated and most down-regulated genes upon target gene perturbation identified in ECCITE-seq data as described in (a). The module scores show the average expression of perturbation-specific target genes per cell comparing cells with the indicated target gene perturbation to cells with non-targeting control gRNAs (one-tailed Kolmogorov–Smirnov test). **c)**

EnrichR gene ontology analysis for biological processes (GOBP) for all single-gene perturbations ($n = 28$) using up to 100 significantly ($p < 0.01$, Wilcoxon's rank sum test) upregulated genes per gene pair compared to NT condition. Shown are the $-\log_{10}$ -transformed adjusted p-values for GO-terms with $p < 0.00001$ (Fisher's exact test) in at least one condition. **d-h)** Comparison of transcriptional responses for double versus single perturbation. Heatmaps show deviation in average gene expression relative to unperturbed cells for the 20 most significantly regulated genes (Wilcoxon's rank sum test). These heatmaps visualize a range of observed interactions between gene pairs, including cases where genes contribute equally to the dual perturbation response (d-f), and where one gene's perturbation signature dominates over the other (g-h). Average heatmaps in g is accompanied by single-cell gene expression heatmap below.



Extended Data Fig. 9 | Structured RNAs can improve bcgRNA detection in CaRPool-seq experiments. a) Nucleotide sequences that can form stable RNA structures when placed 3' to a bcgRNA. Sequences found in MALAT1 and NEAT1 (MEN β) required nucleotide exchanges (shown in red) to remove potential terminator sequences ($\geq 4U$) and allow the sequences to be fully transcribed by RNA polymerase III. **b)** Violin plots depicting protein expression of target genes (ADT UMI counts for CD46, CD55, CD71), grouped by CRISPR arrays [combination of target gene (y-axis) and stabilizing RNA element (x-axis)]; (total cells: $n = 1,770$; conditions $n = 28$; cell per condition: median $n = 63$ cells; s.d. $n = 30$ cells). Three dashed lines indicate 50%, 25%, and 12.5% UMI count relative to the mean of all non-targeting cells by target ADT. The numbers above each violin plot indicate

the median reduction across single cells for cells with matching gRNA and target. Diamonds indicate median value of cell population. **c)** Fold enrichment of bcgRNA UMI counts relative to UMI counts in the standard bcgRNA capture condition separated by the target gene. The evopreQ1 element yielded on average 6-fold higher bcgRNA detection sensitivity ($n = 4$ per condition). Bars indicate mean. **d)** UMI Fraction comparing the assigned bcgRNA to the sum of assigned and second most abundant bcgRNA that may be detected for the same cell [UMI g1 / (UMI g1 + UMI g2)]. Boxes indicate the median and interquartile ranges, with whiskers indicating 1.5 times the interquartile range. (Total cells: $n = 1,770$; conditions $n = 28$; cell per condition: median $n = 63$ cells; s.d. $n = 30$ cells).

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- A description of all covariates tested
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- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

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Software and code

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Data collection

Single cell data processing
RNA and bcgRNA UMI count matrices were generated from raw sequencing data using CellRanger (v3.0.1, v4.0.0 or v6.0.0, as indicated)
HTO and ADT UMI count matrices were acquired using CiteSeqCount (v1.4.2).
Pooled screen data processing further used:
custom scripts for read processing and demultiplexing (<https://github.com/hwessels/Cas13>)
bowtie v1.1.2
fastx-tools/0.0.14
Details as stated in the material and methods section.
Bulk RNA-seq:
Drop-seq tools v1.0

Data analysis

FACS:
FlowJo (v10) and R (v3.6) was used for FACS data analysis.
Pooled screen data analysis:
R v3.6.0
RobustRankAggreg v1.1 (R package)
SVA v3.34.0 (R package)
Single cell data analysis:
R v.4.1.0
Seurat (v4).
energy v1.7-10 (R package)
MASS v7.3-58.1 (R package)
destiny 3.8.1 (R package)
monocle3 1.2.4 (R package)
See Method section within for a detailed description.

Other:
blast v2.6.0

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Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

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For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	CaRPool-seq has been performed profiling: 2,387 HEK293FT or NIH/3T3 cells in a species mixing experiment 9,355 HEK293FT cells targeting cell surface proteins 52,496 THP1 cells in the AML differentiation experiment 3,036 HEK293FT cells comparing stabilizing RNA elements In addition, we profiled 13,947 cells in the direct capture Perturb-seq experiment. Cell numbers reflect cell barcodes returned from CellRanger, filtered for HTO singlets. All pooled screens have been conducted with a coverage of >1000x at all times. Similarly, we stained at least 1000x coverage of cells prior to fluorescent activated cell sorting.
Data exclusions	Single cell data processing is described in detail in the method section. In brief, we used cell hashing to mark individual samples within an experiment and to identify singlet cells. Only these cells were retained. For downstream analysis, we only retained cells with the expected number of expected sgRNA (#1-3) or bcgRNA (#1) features. Additional filtering based on the number of cells per condition is described in the text where applicable.
Replication	All FACS experiments have been performed in three independent replicate experiments. Replicate experiments generally agreed. The Cas13 single gRNA pooled screen was performed using 10 gRNAs per gene. We used Robust Rank Aggregation to verify reproducibility across gRNA. Each analyzed perturbation in the pooled single-cell CRISPR screens was present with at least 25 cells. In the THP1 cell CaRPool-seq experiment, we included an independent technical replicate (alternative gRNAs) for each single and double perturbation. We removed guides RNA g2 GF11, as it failed to reproduce the GF11 g1 response.
Randomization	It is not relevant since this is a single cell study
Blinding	It is not relevant since this is a single cell study

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involvement in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input type="checkbox"/>	<input checked="" type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used

FACS (vendor BioLegend)
 CD46 #352405 clone TRA-2-10 (3µl per 1x10⁶ cells in 100µl),
 CD55 #311311 clone JS11 (5µl per 1x10⁶ cells in 100µl),
 CD71 (TFRC) #334105 clone CYIG4 (4µl per 1x10⁶ cells in 100µl)
 CD11b clone ICRF44 #301322 (2µl per 1x10⁶ cells in 100µl)
 Pooled screen (vendor BioLegend)
 CD11b clone ICRF44 #301322 (4µl per 1x10⁶ cells per 100µl)
 CD14 clone HCD14 #325608 (4µl per 1x10⁶ cells per 100µl)
 CITE-seq (vendor BioLegend; stable IDs provided)
 CD9 TotalSeq™-A0579
 CD11a TotalSeq™-A0185
 CD11b TotalSeq™-A0161
 CD11c TotalSeq™-A0053
 CD16 TotalSeq™-A0083
 CD29 TotalSeq™-A0369
 CD33 TotalSeq™-A0052
 CD45RA TotalSeq™-A0063
 CD46 TotalSeq™-A0858
 CD52 TotalSeq™-A0033
 CD55 TotalSeq™-A0383
 CD56 TotalSeq™-A0047
 CD59 TotalSeq™-A0361
 CD63 TotalSeq™-A0404
 CD71 TotalSeq™-A0394
 CD123 TotalSeq™-A0064
 CD127 TotalSeq™-A0390
 CD135 TotalSeq™-A0351
 CD183 TotalSeq™-A0140
 CD185 TotalSeq™-A0144
 HLA-DR TotalSeq™-A0159
 IgM TotalSeq™-A0136
 Cell Hashing (vendor BioLegend; stable IDs provided)
 HTO_01 TotalSeq™-A0251
 HTO_02 TotalSeq™-A0252
 HTO_03 TotalSeq™-A0253
 HTO_04 TotalSeq™-A0254
 HTO_05 TotalSeq™-A0255
 HTO_06 TotalSeq™-A0256
 HTO_07 TotalSeq™-A0257
 HTO_08 TotalSeq™-A0258
 HTO_10 TotalSeq™-A0260
 Purified anti-human β2-microglobulin [2M2] #316302
 anti-CD298 clone:LNH-94 #341712

Validation

Antibodies were validated by the vendors. All antigens used were validated before. An extended list is available from the vendor. Please find all validation data on <https://www.biolegend.com>

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)

HEK293FT cells were acquired from ThermoFisher (R70007) and NIH/3T3 and THP1 cells were acquired from ATCC (CRL-1658, TIB-202).

Authentication

All cell lines used have been authenticated by the vendors. We do not perform authentication by ourselves. For detail, please inquire with the vendor.

Mycoplasma contamination

All cell lines were tested as mycoplasma-free using Lonza MycoAlert (#LT07-518).

Commonly misidentified lines
(See [ICLAC](#) register)

No commonly misidentified cell lines were used.

Flow Cytometry

Plots

Confirm that:

- The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- All plots are contour plots with outliers or pseudocolor plots.
- A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

Cells were stained for the respective cell surface protein for 30 min at 4°C and measured or sorted by fluorescence-activated cell sorting. THP1 cells were blocked with FxC blocking solution prior to staining for flow cytometry and CITE-seq.

Instrument

Flow cytometry data acquisition and sorting were performed on a Sony SH800 sorter.

Software

FlowJo (Threestar) was used for flow cytometry data analysis, followed by R for cell sampling and plotting.

Cell population abundance

For Flow cytometry data acquisition we analyzed at least 5,000 gated cells per sample. If cell numbers varied, we always sampled (randomly) all samples to the same number of cells.

For fluorescent activated cell sorting based pooled screens, we collecting input representations of at least 1000x coverage per (bc)gRNA and stained cells with at least a 1000x coverage per (bc)gRNA. Sorted population ranged from 1.0×10^6 to 1.5×10^6 cells per sample.

Gating strategy

For flow cytometry analysis and pooled screens, cells were gated by forward and side scatter and signal intensity to remove potential multiplets. If present, cells were additionally gated with a live-dead staining (LIVE/DEAD Fixable Violet Dead Cell Stain Kit, Thermo Fisher L34963 or DAPI, Sigma - 0.4µg per ml PBS). For pooled screen sample collection, we sorted cells into the lowest 10-15% (=low) and highest 10-15% (high) bins.

Exemplified gating strategies are provided in the source data file.

- Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.